Access DB# 80754

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner # :_____ Date: _____
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Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 – 703-308-4498
jan.delaval@uspto.gov

****

STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher: Jan	NA Sequence (#)_____	STN _____
Searcher Phone #: 4499	AA Sequence (#) ✓	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: 4/20/02	Bibliographic _____	Dr.Link _____
Date Completed: 4/21/02	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems ✓
Clerical Prep Time: 10	Patent Family _____	WWW/Internet _____
Online Time: 1:12	Other _____	Other (specify) _____

PTO-1590 (8-01)

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:21 ; Search time 26.8182 Seconds
(without alignments)
879.454 Million cell updates/sec

Title: US-09-787-494-2
Perfect score: 984
Sequence: 1 MTMITDSLAVVLQRRDWENP.....LPGPSDTPILPQTSHHHHHH 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
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2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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16: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	976	99.2	176	21	AAY57315	Human betahCG/beta
2	894.5	90.9	252	21	AAY57316	Alpha-mating facto
3	795	80.8	209	20	AAY43299	HCG beta subunit-J
4	795	80.8	212	20	AAY43304	HCG beta subunit-J
5	795	80.8	265	22	AAU04602	Single chain gonad
6	795	80.8	265	22	AAU04614	Single chain gonad
7	795	80.8	265	22	AAE04474	Human single chain
8	795	80.8	265	22	AAE04486	Human single chain
9	793	80.6	145	20	AAW93434	Human hCG beta-sub
10	793	80.6	145	20	AAW95520	Human chorionic go
11	793	80.6	145	21	AAB20558	Human chorionic go
12	793	80.6	145	22	AAU04619	Human chorionic go
13	793	80.6	145	22	AAE04491	Human chorionic go
14	793	80.6	145	22	AAU00709	Beta-subunit of Hu
15	793	80.6	145	22	AAU01139	Human chorionic go
16	793	80.6	145	22	AAB71765	Beta-human chorion
17	793	80.6	145	22	AAB04121	Beta subunit of hu
18	793	80.6	145	23	AAM50776	Human chorionic go
19	793	80.6	145	23	AAU83014	Beta-human chorion
20	793	80.6	165	12	AAR15043	Human chorionic go
21	793	80.6	165	20	AAY05748	Human chorionic go
22	793	80.6	165	20	AAW99533	Human chorionic go
23	793	80.6	165	21	AAB15358	Human chorionic go
24	793	80.6	165	22	AAB49896	Human chorionic go
25	793	80.6	165	23	AAU96134	Human chorionic go
26	793	80.6	203	20	AAY43298	HCG beta subunit-J
27	793	80.6	206	20	AAY43303	HCG beta subunit-J
28	793	80.6	273	20	AAY43285	HCG beta subunit-J
29	793	80.6	273	20	AAY43292	HCG beta subunit-J
30	791	80.4	212	20	AAY43278	Human CG beta subu
31	790	80.3	165	19	AAW47473	Human beta-hCG pro
32	790	80.3	165	19	AAW33639	Human chorionic go
33	790	80.3	165	19	AAW33637	Human chorionic go
34	789	80.2	145	20	AAW99530	Human chorionic go
35	789	80.2	165	20	AAW99508	Glycoprotein hormo
36	789	80.2	181	22	AAU04613	Gonadotropin analo
37	789	80.2	181	22	AAE04485	Human single chain
38	788.5	80.1	144	12	AAR15178	hCG histidine subs
39	788	80.1	145	12	AAR15171	hCG methionine sub
40	788	80.1	145	12	AAR15173	hCG histidine subs
41	788	80.1	165	20	AAW99514	Glycoprotein hormo
42	788	80.1	165	20	AAW99507	Glycoprotein hormo
43	788	80.1	165	20	AAW99509	Glycoprotein hormo
44	787	80.0	145	12	AAR15169	hCG methionine sub
45	787	80.0	145	14	AAR30999	Human chorionic go

ALIGNMENTS

RESULT 1
AAY57315
ID AAY57315 standard; Protein; 176 AA.
XX
AC AAY57315;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human betahCG/beta-gal fusion protein.
XX
KW Human chorionic gonadotropin; hCG; betahCG; vaccine; chitosan;
KW infertility; betahCG/beta-gal; fusion protein.
XX
OS Homo sapiens.
XX
PN WO200015253-A1.
XX
PD 23-MAR-2000.
XX
PF 16-SEP-1999; 99WO-US21591.
XX
PR 17-SEP-1998; 98US-0100766.
XX
PA (ZONA-) ZONAGEN INC.
XX
PI Harris J, Martinez M;
XX
DR WPI; 2000-271258/23.
DR N-PSDB; AAZ90609.
XX
PT Novel human beta-subunit chorionic gonadotropin vaccines used to
PT interrupt fertility in mammals by the immunological inactivation of the
PT pregnancy hormone chorionic gonadotropin -

```
XX
PS   Claim 5; Page 32-33; 39pp; English.
XX
CC   The invention provides novel vaccine compositions which comprise the
CC   beta-subunit of human chorionic gonadotropin (betahCG)in combination
CC   with chitosan-based adjuvants. The vaccines are used to induce
CC   infertility especially transient infertility, in female mammals. The
CC   compositions are also used for antibody production. The vaccines comprise
CC   a well-tolerated chitosan-based adjuvant which induces the production of
CC   anti-chorionic gonadotropin antibodies, without inducing the side effects
CC   (e.g. hypersensitivity, erythema, etc.) associated with other adjuvants.
CC   The vaccine also overcomes the problem of non-responsiveness in some
CC   individuals. The present sequence represents a betahCG/beta-gal fusion
CC   protein consisting of leaderless betahCG linked to a beta-gal fragment.
XX
SQ   Sequence   176 AA;

  Query Match             99.2%;  Score 976;  DB 21;  Length 176;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-70;
  Matches  176;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MTMITDSLAVVLQRRDWENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MTMITDSLAVVLQRRDWENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAG 60

Qy      61 YCPTMTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YCPTMTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRS 120

Qy     121 TTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQTSHHHHH 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQTSHHHHH 176


RESULT 2
AAY57316
ID   AAY57316 standard; Protein; 252 AA.
XX
AC   AAY57316;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Alpha-mating factor fragment/betahCG fusion protein.
XX
KW   Human chorionic gonadotropin; hCG; betahCG; vaccine; chitosan;
KW   infertility; betahCG/beta-gal; fusion protein.
XX
OS   Homo sapiens.
XX
PN   WO200015253-A1.
XX
PD   23-MAR-2000.
XX
PF   16-SEP-1999;   99WO-US21591.
XX
PR   17-SEP-1998;   98US-0100766.
XX
PA   (ZONA-) ZONAGEN INC.
XX
PI   Harris J,  Martinez M;
XX
DR   WPI; 2000-271258/23.
DR   N-PSDB; AAZ90610.
XX
PT   Novel human beta-subunit chorionic gonadotropin vaccines used to
PT   interrupt fertility in mammals by the immunological inactivation of the
PT   pregnancy hormone chorionic gonadotropin  -
XX
PS   Claim 5; Page 34-35; 39pp; English.
XX
CC   The invention provides novel vaccine compositions which comprise the
CC   beta-subunit of human chorionic gonadotropin (betahCG)in combination
CC   with chitosan-based adjuvants. The vaccines are used to induce
CC   infertility especially transient infertility, in female mammals. The
CC   compositions are also used for antibody production. The vaccines comprise
CC   a well-tolerated chitosan-based adjuvant which induces the production of
CC   anti-chorionic gonadotropin antibodies, without inducing the side effects
CC   (e.g. hypersensitivity, erythema, etc.) associated with other adjuvants.
CC   The vaccine also overcomes the problem of non-responsiveness in some
CC   individuals. The present sequence represents a betahCG fragment
CC   fused to an alpha-mating factor leader sequence at the N-terminus.
XX
SQ   Sequence   252 AA;

  Query Match             90.9%;  Score 894.5;  DB 21;  Length 252;
  Best Local Similarity   93.6%;  Pred. No. 9.9e-64;
  Matches  162;  Conservative    4;  Mismatches    2;  Indels    5;  Gaps    1;

Qy      10 VVLQRRDWE-----NPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPT 64
           | |::|: |     :||||||||||||||||||||||||||||||||||||||||||||
Db      80 VSLEKREAEAYVEFDPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPT 139

Qy      65 MTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 124
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     140 MTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 199

Qy     125 GGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQTSHHHHHH 177
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     200 GGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQTSHHHHHH 252


RESULT 3
AAY43299
ID   AAY43299 standard; Protein; 209 AA.
XX
AC   AAY43299;
XX
DT   19-JAN-2000  (first entry)
XX
DE   HCG beta subunit-Jun fusion protein sequence.
XX
KW   Cysteine knot protein; protein formation; heterodimeric protein analog;
KW   deglycosylated glycoprotein hormone; infertility; immunogen; antigen;
KW   polycystic ovarian disease; hCG; human; chorionic gonadotrophin;
KW   beta subunit; therapy; Jun.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9953065-A1.
XX
PD   21-OCT-1999.
XX
PF   13-APR-1999;   99WO-US08018.
XX
PR   14-APR-1998;   98US-0059625.
XX
PA   (UYNE-) UNIV NEW JERSEY.
XX
PI   Moyle WR;
XX
DR   WPI; 1999-620431/53.
XX
PT   Methods for producing heterodimers, particularly analogues of hormones,
PT   from subunits of cysteine knot proteins -
XX
PS   Example 7; Fig 20; 73pp; English.
XX
CC   This sequence is a fusion protein of HCG and Jun. The invention
CC   relates to a method of forming a cysteine knot protein (I) having alpha
CC   and beta-subunits comprising attaching a dimerisation domain (DD) to
CC   either the N-termini of both subunits or the N-terminus of the
CC   alpha-subunit and to the C-terminus of the beta-subunit and dimerising
CC   the products to form a heterodimeric protein analog (II). The method is
CC   used to produce analogues (agonists or antagonists) of deglycosylated
CC   glycoprotein hormones, potentially useful, e.g. for treating infertility
```

CC where caused by polycystic ovarian disease (associated with excessive
CC levels of luteinising hormone). Products that retain DD's are also useful
CC as immunogens or antigens (since a DD may containing highly antigenic
CC amino acid sequences). Attachment of a DD (which may be removed later)
CC facilitates the formation of heterodimers, that have similar structures
CC (and thus receptor-binding and immunogenic properties) to native dimers,
CC and allows the combination of subunits that would otherwise combine
CC poorly, or not at all. The N-terminal part of a glycoprotein hormone may
CC be modified without loss of activity, and attachment of the DD reduces
CC formation of homodimers. Heterodimers have longer circulation times in
CC vivo than individual subunits.
XX
SQ Sequence 209 AA;

Query Match 80.8%; Score 795; DB 20; Length 209;
Best Local Similarity 99.3%; Pred. No. 6.9e-56;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy 86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy 146 KAPPPSLPSPSRLPGPSDTPILPQTS 171
|||||||||||||||||||||||| |
Db 142 KAPPPSLPSPSRLPGPSDTPILPQGS 167

RESULT 4
AAY43304
ID AAY43304 standard; Protein; 212 AA.
XX
AC AAY43304;
XX
DT 19-JAN-2000 (first entry)
XX
DE HCG beta subunit-Jun fusion protein sequence.
XX
KW Cysteine knot protein; protein formation; heterodimeric protein analog;
KW deglycosylated glycoprotein hormone; infertility; immunogen; antigen;
KW polycystic ovarian disease; hCG; human; chorionic gonadotrophin;
KW beta subunit; therapy; Jun.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9953065-A1.
XX
PD 21-OCT-1999.
XX
PF 13-APR-1999; 99WO-US08018.
XX
PR 14-APR-1998; 98US-0059625.
XX
PA (UYNE-) UNIV NEW JERSEY.
XX
PI Moyle WR;
XX
DR WPI; 1999-620431/53.
XX
PT Methods for producing heterodimers, particularly analogues of hormones,
PT from subunits of cysteine knot proteins -
XX
PS Example 7; Fig 20; 73pp; English.
XX
CC This sequence is a fusion protein of HCG and Jun. The invention
CC relates to a method of forming a cysteine knot protein (I) having alpha
CC and beta-subunits comprising attaching a dimerisation domain (DD) to
CC either the N-termini of both subunits or the N-terminus of the
CC alpha-subunit and to the C-terminus of the beta-subunit and dimerising
CC the products to form a heterodimeric protein analog (II). The method is
CC used to produce analogues (agonists or antagonists) of deglycosylated
CC glycoprotein hormones, potentially useful, e.g. for treating infertility
CC where caused by polycystic ovarian disease (associated with excessive
CC levels of luteinising hormone). Products that retain DD's are also useful
CC as immunogens or antigens (since a DD may containing highly antigenic
CC amino acid sequences). Attachment of a DD (which may be removed later)
CC facilitates the formation of heterodimers, that have similar structures
CC (and thus receptor-binding and immunogenic properties) to native dimers,
CC and allows the combination of subunits that would otherwise combine
CC poorly, or not at all. The N-terminal part of a glycoprotein hormone may
CC be modified without loss of activity, and attachment of the DD reduces
CC formation of homodimers. Heterodimers have longer circulation times in
CC vivo than individual subunits.
XX
SQ Sequence 212 AA;

Query Match 80.8%; Score 795; DB 20; Length 212;
Best Local Similarity 99.3%; Pred. No. 7e-56;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy 86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy 146 KAPPPSLPSPSRLPGPSDTPILPQTS 171
|||||||||||||||||||||||| |
Db 142 KAPPPSLPSPSRLPGPSDTPILPQGS 167

RESULT 5
AAU04602
ID AAU04602 standard; Protein; 265 AA.
XX
AC AAU04602;
XX
DT 23-OCT-2001 (first entry)
XX
DE Single chain gonadotropin analogue #1.
XX
KW Human; glycoprotein hormone; infertility; in vivo fertilisation;
KW single chain gonadotropin.
XX
OS Homo sapiens.
XX
PN US6242580-B1.
XX
PD 05-JUN-2001.
XX
PF 31-MAR-1999; 99US-0282357.
XX
PR 25-AUG-1997; 97US-0918288.
PR 18-FEB-1994; 94US-0199382.
PR 12-AUG-1994; 94US-0289396.
PR 22-SEP-1994; 94US-0310590.
PR 04-NOV-1994; 94US-0334628.
PR 07-DEC-1994; 94US-0351591.
PR 07-JUN-1995; 95US-0475049.
PR 09-MAY-1997; 97US-0853524.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Boime I, Moyle WR;
XX
DR WPI; 2001-424301/45.
DR N-PSDB; AAS08485.
XX
PT New single chain forms of the glycoprotein hormone quartet useful for
PT generating antibodies specifically immunoreactive with the new

PT compounds, in treating infertility, or as aids for in vivo
PT fertilization techniques -
XX
PS Example 5; Fig 5; 86pp; English.
XX
CC The sequence represents the amino acid sequence of single chain
CC gonadotropin analogue #1. The glycoprotein hormone analogue is
CC useful for generating antibodies specifically immunoreactive with new
CC compounds, as a substitute for the heterodimeric forms of the hormones,
CC in the treatment of infertility, as an aid for in vivo fertilisation
CC techniques, and in other therapeutic methods associated with the native
CC hormone. The single chain protein is further useful as a reagent in a
CC manner similar to the heterodimer, as a diagnostic tool to detect the
CC presence of antibodies with respect to the native proteins in the
CC biological samples, as a control reagent in assay kits for assessing the
CC levels of these hormones in various samples, and in detecting and
CC purifying receptors to which the native hormones bind. The single chain
CC forms of the heterodimers or homodimers have the following advantages
CC over their dimeric forms: they are more stable, problems of recombinant
CC production are reduced since only a single gene is needed to transcribe,
CC translate and process, provide an alternate form thus permitting fine
CC tuning of activity levels and of in vivo half lives. Single chain forms
CC are unique starting materials for identifying truncated forms with the
CC activity of the dimer. The linkage between the subunits permits the
CC protein to be engineered without disturbing the overall folding of the
CC protein.
XX
SQ Sequence 265 AA;

Query Match 80.8%; Score 795; DB 22; Length 265;
Best Local Similarity 99.3%; Pred. No. 8.7e-56;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQTS 171
           ||||||||||||||||||||||||| |
Db     142 KAPPPSLPSPSRLPGPSDTPILPQGS 167
```

RESULT 6
AAU04614
ID AAU04614 standard; Protein; 265 AA.
XX
AC AAU04614;
XX
DT 23-OCT-2001 (first entry)
XX
DE Single chain gonadotropin analogue #1a.
XX
KW Human; glycoprotein hormone; infertility; in vivo fertilisation;
KW single chain gonadotropin.
XX
OS Homo sapiens.
XX
PN US6242580-B1.
XX
PD 05-JUN-2001.
XX
PF 31-MAR-1999; 99US-0282357.
XX
PR 25-AUG-1997; 97US-0918288.
PR 18-FEB-1994; 94US-0199382.
PR 12-AUG-1994; 94US-0289396.
PR 22-SEP-1994; 94US-0310590.
PR 04-NOV-1994; 94US-0334628.
PR 07-DEC-1994; 94US-0351591.
PR 07-JUN-1995; 95US-0475049.
PR 09-MAY-1997; 97US-0853524.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Boime I, Moyle WR;
XX
DR WPI; 2001-424301/45.
DR N-PSDB; AAS08509.
XX
PT New single chain forms of the glycoprotein hormone quartet useful for
PT generating antibodies specifically immunoreactive with the new
PT compounds, in treating infertility, or as aids for in vivo
PT fertilization techniques -
XX
PS Example 16; Fig 17; 86pp; English.
XX
CC The sequence represents the amino acid sequence of single chain
CC gonadotropin analogue #1a. The glycoprotein hormone analogue is
CC useful for generating antibodies specifically immunoreactive with new
CC compounds, as a substitute for the heterodimeric forms of the hormones,
CC in the treatment of infertility, as an aid for in vivo fertilisation
CC techniques, and in other therapeutic methods associated with the native
CC hormone. The single chain protein is further useful as a reagent in a
CC manner similar to the heterodimer, as a diagnostic tool to detect the
CC presence of antibodies with respect to the native proteins in the
CC biological samples, as a control reagent in assay kits for assessing the
CC levels of these hormones in various samples, and in detecting and
CC purifying receptors to which the native hormones bind. The single chain
CC forms of the heterodimers or homodimers have the following advantages
CC over their dimeric forms: they are more stable, problems of recombinant
CC production are reduced since only a single gene is needed to transcribe,
CC translate and process, provide an alternate form thus permitting fine
CC tuning of activity levels and of in vivo half lives. Single chain forms
CC are unique starting materials for identifying truncated forms with the
CC activity of the dimer. The linkage between the subunits permits the
CC protein to be engineered without disturbing the overall folding of the
CC protein.
XX
SQ Sequence 265 AA;

Query Match 80.8%; Score 795; DB 22; Length 265;
Best Local Similarity 99.3%; Pred. No. 8.7e-56;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQTS 171
           ||||||||||||||||||||||||| |
Db     142 KAPPPSLPSPSRLPGPSDTPILPQGS 167
```

RESULT 7
AAE04474
ID AAE04474 standard; Protein; 265 AA.
XX
AC AAE04474;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human single chain gonadotropin analog no:1.
XX
KW Human; single chain gonadotropin analog no:1; anti-infertility; drug;
KW peptide therapy; luteinising hormone; LH; follicle stimulating hormone;
KW FSH; thyroid stimulating hormone; TSH; chorionic gonadotropin; CG;
KW glycoprotein; infertility; fusion protein.
XX

```
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          21..165
FT                   /note= "Corresponds to 1-145 amino acids of human
FT                   chorionic gonadotropin (CG) beta-subunit"
FT   Region          166..173
FT                   /note= "Linker peptide"
FT   Region          174..265
FT                   /note= "Corresponds to 1-92 amino acids of human single
FT                   chain gonadotropin alpha-subunit"
XX
PN   US6238890-B1.
XX
PD   29-MAY-2001.
XX
PF   25-AUG-1997;   97US-0918288.
XX
PR   18-FEB-1994;   94US-0199382.
PR   12-AUG-1994;   94US-0289396.
PR   22-SEP-1994;   94US-0310590.
PR   04-NOV-1994;   94US-0334628.
PR   07-DEC-1994;   94US-0351591.
PR   07-JUN-1995;   95US-0475049.
PR   09-MAY-1997;   97US-0853524.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Boime I,  Moyle WR;
XX
DR   WPI; 2001-366474/38.
DR   N-PSDB; AAD08785.
XX
PT   New DNA or RNA encoding single chain protein useful in treating
PT   infertility, as aids in vitro fertilization techniques, or other
PT   therapeutic methods associated with the native hormones  -
XX
PS   Claim 9; Fig 5; 87pp; English.
XX
CC   The invention relates to human single chain forms of the glycoprotein
CC   hormone quartet which is an agonist or antagonist of luteinising hormone
CC   (LH), follicle stimulating hormone (FSH), thyroid stimulating hormone
CC   (TSH) or chorionic gonadotropin (CG). All these hormones are heterodimers
CC   having identical alpha subunits and differing beta subunits. The agonist
CC   forms of single chain hormones are used in treating infertility, as aids
CC   in vitro fertilisation techniques, and other therapeutic methods
CC   associated with the native hormones. The single chain hormones are useful
CC   as reagents in a manner similar to heterodimers, as diagnostic tools to
CC   detect the presence of antibodies with respect to the native proteins in
CC   biological samples, as control reagents in assay kits for assessing the
CC   levels of these hormones in various samples, in detecting and purifying
CC   receptors to which the native hormones bind. The single chain hormones
CC   are also used in affinity chromatographic preparation of receptors or
CC   antihormone antibodies. They are used as purification tools for
CC   isolation of subsequent preparations of these materials and to monitor
CC   levels of single chain hormones administered as drugs. The single chain
CC   glycoproteins are used to generate antibodies specifically immunoreactive
CC   with these new compounds, as substitutes for the heterodimeric forms of
CC   hormones. The present sequence is human single chain gonadotropin analog
CC   no:1 related to the invention. Analog no:1 is a fusion protein consisting
CC   of human chorionic gonadotropin (CG) beta-subunit (1-145 amino acids)
CC   fused to human single chain gonadotropin alpha-subunit (1-92 amino acids)
CC   by a linker sequence. This analog serves as a useful starting compound
CC   for template directed vaccine design and for the development of hormone-
CC   specific vaccines for use in humans.
XX
SQ   Sequence   265 AA;

  Query Match             80.8%;  Score 795;  DB 22;  Length 265;
  Best Local Similarity   99.3%;  Pred. No. 8.7e-56;
  Matches  145;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQTS 171
           |||||||||||||||||||||||| |
Db     142 KAPPPSLPSPSRLPGPSDTPILPQGS 167


RESULT 8
AAE04486
ID   AAE04486 standard; Protein; 265 AA.
XX
AC   AAE04486;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human single chain gonadotropin analog no:1a.
XX
KW   Human; single chain gonadotropin analog no:1a; anti-infertility; drug;
KW   peptide therapy; luteinising hormone; LH; follicle stimulating hormone;
KW   FSH; thyroid stimulating hormone; TSH; chorionic gonadotropin; CG;
KW   glycoprotein; infertility; fusion protein; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          21..165
FT                   /note= "Corresponds to 1-145 amino acids of human
FT                   chorionic gonadotropin (CG) beta-subunit"
FT   Region          166..173
FT                   /note= "Linker peptide"
FT   Region          174..265
FT                   /note= "Corresponds to 1-92 amino acids of human single
FT                   chain gonadotropin alpha-subunit"
FT   Misc-difference 225
FT                   /note= "Wild type Asn substituted with Gln"
FT   Misc-difference 251
FT                   /note= "Wild type Asn substituted with Gln"
XX
PN   US6238890-B1.
XX
PD   29-MAY-2001.
XX
PF   25-AUG-1997;   97US-0918288.
XX
PR   18-FEB-1994;   94US-0199382.
PR   12-AUG-1994;   94US-0289396.
PR   22-SEP-1994;   94US-0310590.
PR   04-NOV-1994;   94US-0334628.
PR   07-DEC-1994;   94US-0351591.
PR   07-JUN-1995;   95US-0475049.
PR   09-MAY-1997;   97US-0853524.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Boime I,  Moyle WR;
XX
DR   WPI; 2001-366474/38.
DR   N-PSDB; AAD08809.
XX
PT   New DNA or RNA encoding single chain protein useful in treating
PT   infertility, as aids in vitro fertilization techniques, or other
PT   therapeutic methods associated with the native hormones  -
XX
PS   Claim 9; Fig 17; 87pp; English.
XX
CC   The invention relates to human single chain forms of the glycoprotein
```

```
CC   hormone quartet which is an agonist or antagonist of luteinising hormone
CC   (LH), follicle stimulating hormone (FSH), thyroid stimulating hormone
CC   (TSH) or chorionic gonadotropin (CG). All these hormones are heterodimers
CC   having identical alpha subunits and differing beta subunits. The agonist
CC   forms of single chain hormones are used in treating infertility, as aids
CC   in vitro fertilisation techniques, and other therapeutic methods
CC   associated with the native hormones. The single chain hormones are useful
CC   as reagents in a manner similar to heterodimers, as diagnostic tools to
CC   detect the presence of antibodies with respect to the native proteins in
CC   biological samples, as control reagents in assay kits for assessing the
CC   levels of these hormones in various samples, in detecting and purifying
CC   receptors to which the native hormones bind. The single chain hormones
CC   are also used in affinity chromatographic preparation of receptors or
CC   antihormone antibodies. They are used as purification tools for
CC   isolation of subsequent preparations of these materials and to monitor
CC   levels of single chain hormones administered as drugs. The single chain
CC   glycoproteins are used to generate antibodies specifically immunoreactive
CC   with these new compounds, as substitutes for the heterodimeric forms of
CC   hormones. The present sequence is human single chain gonadotropin analog
CC   no:1a related to the invention. Analog no:1a is a fusion protein
CC   consisting of human chorionic gonadotropin (CG) beta-subunit (1-145 amino
CC   acids) fused to human single chain gonadotropin alpha-subunit (1-92 amino
CC   acids) by a linker sequence. This analog serves as a useful starting
CC   compound for template directed vaccine design and for the development of
CC   hormone-specific vaccines for use in humans.
XX
SQ   Sequence   265 AA;

  Query Match             80.8%;  Score 795;  DB 22;  Length 265;
  Best Local Similarity   99.3%;  Pred. No. 8.7e-56;
  Matches  145;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQTS 171
           ||||||||||||||||||||||||| |
Db     142 KAPPPSLPSPSRLPGPSDTPILPQGS 167


RESULT 9
AAW93434
ID   AAW93434 standard; peptide; 145 AA.
XX
AC   AAW93434;
XX
DT   11-JUN-1999  (first entry)
XX
DE   Human hCG beta-subunit peptide structure I.
XX
KW   Human chorionic gonadotropin; beta subunit; antigenic peptide; hCG;
KW   contraceptive; vaccine; fertility; polyclonal antisera; diagnostic;
KW   immunogen; human luteinising hormone.
XX
OS   Homo sapiens.
XX
PN   US5891992-A.
XX
PD   06-APR-1999.
XX
PF   06-JUN-1995;   95US-0467569.
XX
PR   07-AUG-1989;   89US-0390530.
PR   04-DEC-1985;   85US-0804642.
PR   17-AUG-1987;   87US-0086401.
PR   06-OCT-1992;   92US-0958601.
PR   06-JUN-1995;   95US-0467569.
XX
PA   (OHIS ) UNIV OHIO STATE RES FOUND.
XX
PI   Stevens VC;
XX
DR   WPI; 1999-253928/21.
XX
PT   Synthetic antigenic peptides from human chorionic gonadotropin
PT   beta-subunit
XX
PS   Disclosure; Column 19; 80pp; English.
XX
CC   This invention describes novel synthetic antigenic peptides (A) based
CC   on the human chorionic gonadotropin (hCG) beta-subunit. These peptides
CC   have contraceptive properties and are used for the development of
CC   vaccines used to control fertility in animals and to generate
CC   polyclonal antisera for diagnostic use. The peptides are more specific
CC   immunogens than corresponding unmodified peptides from hCG beta-subunit,
CC   i.e. they do not elicit antibodies that cross-react with human
CC   luteinising hormone.
XX
SQ   Sequence   145 AA;

  Query Match             80.6%;  Score 793;  DB 20;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 7e-56;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
           |||||||||||||||||||||||||
Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 10
AAW95520
ID   AAW95520 standard; protein; 145 AA.
XX
AC   AAW95520;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Human chorionic gonadotrophin (hCG) beta subunit.
XX
KW   Human; chorionic gonadotropin; hCG; three-dimensional; 3D; analogue;
KW   molecular simulation; visual display; chemical structure; growth factor;
KW   N-glycosylation site; follicle stimulating hormone; luteinising hormone;
KW   thyroid stimulating hormone; in vitro fertilisation; fertility; mutation;
KW   beta subunit; glycoprotein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 64
FT                   /note= "wild-type Phe at this position can be mutated
FT                           to Asn to introduce a new N-glycosylation site;
FT                           see claim 3"
FT   Misc-difference 79
FT                   /note= "wild-type Val at this position can be mutated
FT                           to Asn to introduce a new N-glycosylation site;
FT                           see claim 3"
XX
PN   US5864488-A.
XX
PD   26-JAN-1999.
XX
PF   24-FEB-1995;   95US-0395238.
XX
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```
PR   24-FEB-1994;   94GB-0003600.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Grootenhuis PDJ,  Harris DC,  Isaacs NW,  Lapthorn AJ;
XX
DR   WPI; 1999-131522/11.
XX
PT   Determining the 3-dimensional coordinates of chorionic gonadotrophin
PT   and computer-assisted re-design of the chemical structure - used for
PT   production of gonadotrophin hormone analogues
XX
PS   Examples; Fig 2; 60pp; English.
XX
CC   The invention relates to determining whether an analogue of human
CC   chorionic gonadotropin (hCG) will have an altered three-dimensional (3D)
CC   structure as compared to hCG. Analogues of hCG and other glycoprotein
CC   hormones are produced by inputting chemical changes to the 3D structure
CC   into a computer loaded with 3D molecular simulation software and
CC   representing visually on a computer display. On inputting into the data
CC   input of the computer at least one operator change in chemical structure
CC   of the hCG molecule, the molecular simulation software produces a
CC   modified 3D molecular representation of the analogue structure. The 3D
CC   representation of the analogue can be displayed on the visual display,
CC   whereby changes in 3D structure of the hCG molecule consequent on changes
CC   in chemical structure can be visually determined. Glycoprotein analogues
CC   with additional glycosylation sites, and analogues with non-essential
CC   hairpins deleted can be produced by this method. The methods can be used
CC   to obtain analogues of hCG, follicle stimulating hormone, luteinising
CC   hormone, thyroid stimulating hormone, which may act as agonists or
CC   antagonists. The analogues can be used as growth factors in mammals, for
CC   in vitro fertilisation techniques and for treatment in vivo to enhance
CC   fertility. The present sequence represents the beta subunit of hCG.
CC   N-glycosylation sites can be introduced by single point mutations at
CC   specified positions to produce hCG analogues.
XX
SQ   Sequence   145 AA;

  Query Match             80.6%;  Score 793;  DB 20;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 7e-56;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
           |||||||||||||||||||||||||
Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 11
AAB20558
ID   AAB20558 standard; protein; 145 AA.
XX
AC   AAB20558;
XX
DT   11-DEC-2000  (first entry)
XX
DE   Human chorionic gonadotropin beta subunit amino acid sequence.
XX
KW   Human; chorionic gonadotropin antigen; follicle stimulating hormone;
KW   contraception; abortion; hormone related disease; carcinoma; cytostatic;
KW   contraceptive; antiinfertility; antihypertensive; antidiabetic; vaccine;
KW   fertility; cancer; hypertension; diabetes.
XX
OS   Homo sapiens.
XX
PN   US6096318-A.
XX
PD   01-AUG-2000.
XX
PF   06-JUN-1995;   95US-0466445.
XX
PR   25-AUG-1978;   78US-0936876.
PR   15-JUL-1987;   87US-0073748.
PR   26-AUG-1992;   92US-0935331.
PR   17-FEB-1989;   89US-0311331.
PR   07-MAY-1973;   73US-0357892.
PR   16-OCT-1973;   73US-0406821.
PR   22-APR-1974;   74US-0462955.
PR   14-OCT-1975;   75US-0622031.
PR   16-JAN-1980;   80US-0112628.
PR   20-NOV-1981;   81US-0323690.
PR   18-MAY-1983;   83WO-US00777.
PR   02-NOV-1984;   84US-0667863.
XX
PA   (OHIS ) UNIV OHIO STATE.
XX
PI   Stevens VC;
XX
DR   WPI; 2000-542298/49.
XX
PT   New antigen for treating hormone related diseases, is conjugated with a
PT   specific polypeptide which elicits an antibody response against human
PT   chorionic gonadotropin  -
XX
PS   Disclosure; Column 18; 61pp; English.
XX
CC   The present invention describes an antigen (A) comprising a carrier
CC   chemically conjugated with a polypeptide (I) capable of eliciting
CC   antibody response to human chorionic gonadotropin (CG) and not to human
CC   luteinising hormone (LH), or a polypeptide (II) capable of eliciting
CC   antibody response to human CG. (A) has cytostatic, contraceptive,
CC   antiinfertility, antihypertensive and antidiabetic activities, and can
CC   be used as part of a vaccine. (A) is useful for contraception, abortion
CC   and for treating hormone related diseases, for treating hormone
CC   associated carcinomas and to boost an animals' resistance to exogenous
CC   proteins e.g. viral proteins. (A) is also useful in animal fertility
CC   control, for treating cancer, hypertension, diabetes and related vascular
CC   diseases. (A), safely and effectively controls various disease states
CC   or maladies caused or influenced by unusual excesses of certain
CC   polypeptides such as gastrin, angiotensin II or somatomedian. It also
CC   provides an effective and safe method of terminating a pregnancy soon
CC   after conception which does not have serious harmful side effects.
CC   The present sequence represents the human CG beta subunit amino acid
CC   sequence, which is given in the exemplification of the present
CC   invention.
XX
SQ   Sequence   145 AA;

  Query Match             80.6%;  Score 793;  DB 21;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 7e-56;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
           |||||||||||||||||||||||||
Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 12
AAU04619
ID   AAU04619 standard; protein; 145 AA.
XX
```

```
AC   AAU04619;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human chorionic gonadotropin (hCG) beta, amino acids 1-145.
XX
KW   Human; chorionic gonadotropin; hCG; glycoprotein hormone; infertility;
KW   luteinising hormone; LH; follicle stimulating hormone; FSH;
KW   thyroid stimulating hormone; TH.
XX
OS   Homo sapiens.
XX
PN   US6242580-B1.
XX
PD   05-JUN-2001.
XX
PF   31-MAR-1999;   99US-0282357.
XX
PR   25-AUG-1997;   97US-0918288.
PR   18-FEB-1994;   94US-0199382.
PR   12-AUG-1994;   94US-0289396.
PR   22-SEP-1994;   94US-0310590.
PR   04-NOV-1994;   94US-0334628.
PR   07-DEC-1994;   94US-0351591.
PR   07-JUN-1995;   95US-0475049.
PR   09-MAY-1997;   97US-0853524.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Boime I,  Moyle WR;
XX
DR   WPI; 2001-424301/45.
XX
PT   New single chain forms of the glycoprotein hormone quartet useful for
PT   generating antibodies specifically immunoreactive with the new
PT   compounds, in treating infertility, or as aids for in vivo
PT   fertilization techniques  -
XX
PS   Example 19; Column 34; 86pp; English.
XX
CC   The sequence represents the amino acid sequence of human chorionic
CC   gonadotropin (hCG) beta, amino acids 1-145. The protein is an
CC   important glycoprotein hormone heterodimer, along with luteinising
CC   hormone (LH), follicle stimulating hormone (FSH), thyroid stimulating
CC   hormone (TH), which all have identical alpha subunits but differing beta
CC   subunits. The proteins are useful for generating antibodies specifically
CC   immunoreactive with new compounds, as substitutes for the
CC   heterodimeric forms of the hormones, in the treatment of infertility, as
CC   aids for in vivo fertilisation techniques, and in other therapeutic
CC   methods associated with the native hormones. The single chain proteins
CC   are further useful as reagents in a manner similar to the heterodimers,
CC   as diagnostic tools to detect the presence of antibodies with respect to
CC   the native proteins in the biological samples, as control reagents in
CC   assay kits for assessing the levels of these hormones in various samples,
CC   and in detecting and purifying receptors to which the native hormones
CC   bind. The single chain forms of the heterodimers or homodimers have the
CC   following advantages over their dimeric forms: they are more stable,
CC   problems of recombinant production are reduced since only a single gene
CC   is needed to transcribe, translate and process, provide an alternate form
CC   thus permitting fine tuning of activity levels and of in vivo half lives.
CC   Single chain forms are unique starting materials for identifying
CC   truncated forms with the activity of the dimer. The linkage between the
CC   subunits permits the protein to be engineered without disturbing the
CC   overall folding of the protein.
XX
SQ   Sequence   145 AA;

  Query Match            80.6%;  Score 793;  DB 22;  Length 145;
  Best Local Similarity  100.0%;  Pred. No. 7e-56;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
           |||||||||||||||||||||||||
Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 13
AAE04491
ID   AAE04491 standard; Protein; 145 AA.
XX
AC   AAE04491;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human chorionic gonadotropin beta-subunit fragment (1-145 amino acids).
XX
KW   Human; single chain gonadotropin analog; anti-infertility; drug;
KW   peptide therapy; luteinising hormone; LH; follicle stimulating hormone;
KW   FSH; thyroid stimulating hormone; TSH; chorionic gonadotropin; CG;
KW   glycoprotein; infertility; fusion protein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 145
FT                   /note= "Residue 'O' is present at this location in the
FT                   sequence shown in column 33 of the specification"
XX
PN   US6238890-B1.
XX
PD   29-MAY-2001.
XX
PF   25-AUG-1997;   97US-0918288.
XX
PR   18-FEB-1994;   94US-0199382.
PR   12-AUG-1994;   94US-0289396.
PR   22-SEP-1994;   94US-0310590.
PR   04-NOV-1994;   94US-0334628.
PR   07-DEC-1994;   94US-0351591.
PR   07-JUN-1995;   95US-0475049.
PR   09-MAY-1997;   97US-0853524.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Boime I,  Moyle WR;
XX
DR   WPI; 2001-366474/38.
XX
PT   New DNA or RNA encoding single chain protein useful in treating
PT   infertility, as aids in vitro fertilization techniques, or other
PT   therapeutic methods associated with the native hormones  -
XX
PS   Example 19; Column 103-106; 87pp; English.
XX
CC   The invention relates to human single chain forms of the glycoprotein
CC   hormone quartet which is an agonist or antagonist of luteinising hormone
CC   (LH), follicle stimulating hormone (FSH), thyroid stimulating hormone
CC   (TSH) or chorionic gonadotropin (CG). All these hormones are heterodimers
CC   having identical alpha subunits and differing beta subunits. The agonist
CC   forms of single chain hormones are used in treating infertility, as aids
CC   in vitro fertilisation techniques, and other therapeutic methods
CC   associated with the native hormones. The single chain hormones are useful
CC   as reagents in a manner similar to heterodimers, as diagnostic tools to
CC   detect the presence of antibodies with respect to the native proteins in
CC   biological samples, as control reagents in assay kits for assessing the
CC   levels of these hormones in various samples, in detecting and purifying
CC   receptors to which the native hormones bind. The single chain hormones
CC   are also used in affinity chromatographic preparation of receptors or
```

CC antihormone antibodies. They are used as purification tools for
CC isolation of subsequent preparations of these materials and to monitor
CC levels of single chain hormones administered as drugs. The single chain
CC glycoproteins are used to generate antibodies specifically immunoreactive
CC with these new compounds, as substitutes for the heterodimeric forms of
CC hormones. The present sequence is human chorionic gonadotropin beta-
CC subunit fragment (1-145 amino acids) which is used for constructing
CC single chain gonadotropin analogs related to the invention. Analog
CC fusion proteins serves as useful starting compounds for template directed
CC vaccine design and for the development of hormone-specific vaccines for
CC use in humans.
XX
SQ Sequence 145 AA;

Query Match 80.6%; Score 793; DB 22; Length 145;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy 86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy 146 KAPPPSLPSPSRLPGPSDTPILPQ 169
||||||||||||||||||||||||
Db 122 KAPPPSLPSPSRLPGPSDTPILPQ 145

RESULT 14
AAU00709
ID AAU00709 standard; Protein; 145 AA.
XX
AC AAU00709;
XX
DT 07-SEP-2001 (first entry)
XX
DE Beta-subunit of Human Chorionic Gonadotrophin (HCG).
XX
KW Human chorionic gonadotrophin beta-subunit; HCG; mammal; pregnancy test;
KW human pituitary luteinising hormone; reduced fertility; infertility;
KW contraception; abortion; hormone-associated carcinoma.
XX
OS Homo sapiens.
XX
PN WO200124765-A2.
XX
PD 12-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US27741.
XX
PR 06-OCT-1999; 99US-0413564.
XX
PA (OHIS) UNIV OHIO STATE RES FOUND.
XX
PI Stevens VC;
XX
DR WPI; 2001-328306/34.
XX
PT Peptide analogues of beta-human chorionic gonadotrophin which are able to
PT raise antibodies against human chorionic gonadotrophin are used in
PT vaccines as contraceptives and/or abortificants -
XX
PS Claim 1; Page 35; 214pp; English.
XX
CC The sequence represents the beta-subunit of human chorionic gonadotrophin
CC (betaHCG). Peptide analogues of amino acid residues 38-57 of betaHCG have
CC a disulfide bridge linking the cysteine residues at positions 38 and 57
CC to form a loop structure. The peptides are used in vaccines to raise
CC antibodies against HCG with a significant decrease in antibodies reactive
CC to human pituitary luteinising hormone, to control the biological
CC activity of endogenous HCG. These antibodies may be used in diagnostic
CC tests to determine hormone levels of mammals. The peptides can be used in
CC pregnancy tests and in detection of reduced fertility or infertility.
CC They may also be administered for contraception or abortion processes.
CC Upon conjugation to a foreign carrier, the peptides may be administered
CC to humans to treat hormone-associated carcinomas.
XX
SQ Sequence 145 AA;

Query Match 80.6%; Score 793; DB 22; Length 145;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy 86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy 146 KAPPPSLPSPSRLPGPSDTPILPQ 169
||||||||||||||||||||||||
Db 122 KAPPPSLPSPSRLPGPSDTPILPQ 145

RESULT 15
AAU01139
ID AAU01139 standard; protein; 145 AA.
XX
AC AAU01139;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human chorionic gonadotrophin (HCG) beta-subunit (Structure I).
XX
KW Human chorionic gonadotrophin; HCG; contraception; abortion;
KW hormone-related disorder; hormone-associated carcinoma; cancer; diabetes;
KW vascular disease; Zollinger-Ellison syndrome; chronic digestive disorder;
KW antigenic modification.
XX
OS Homo sapiens.
XX
PN US6217881-B1.
XX
PD 17-APR-2001.
XX
PF 06-JUN-1995; 95US-0467997.
XX
PR 06-OCT-1992; 92US-0958601.
PR 07-AUG-1992; 92US-0390530.
PR 04-DEC-1985; 85US-0804642.
PR 17-AUG-1987; 87US-0086401.
XX
PA (OHIS) UNIV OHIO STATE RES FOUND.
XX
PI Stevens VC;
XX
DR WPI; 2001-289819/30.
XX
PT Novel vaccine composition for provoking the formation of antibodies to
PT human chorionic gonadotropin, contains a peptide comprising disulfide
PT bridges linking terminal cysteine residues to form a loop -
XX
PS Disclosure; Column 19; 82pp; English.
XX
CC The present sequence represents the beta-subunit of human chorionic
CC gonadotrophin (HCG). The HCG beta-subunit polypeptide sequence is
CC used to isolate 3 novel HCG antigenic peptides (AAU01175-AAU01177)
CC with a disulfide bridge linking the terminal cysteine amino acids
CC to form a loop, and conjugated to a carrier. The HCG antigenic
CC peptides can be used in a vaccine composition for provoking an
CC antibody response to HCG in a mammal. The novel HCG antigenic

CC peptides are useful for the purpose of contraception, abortion,
CC and for the treatment of hormone-related disease states and
CC disorders, treatment of hormone-associated carcinomas, and to boost an
CC animal's resistance to exogenous proteins, such as viral proteins. The
CC HCG antigenic peptides are also useful for treating cancer, diabetes,
CC vascular disease, hypertension, Zollinger-Ellison syndrome, and
CC chronic digestive disorders. Also described are various structures
CC (AAU01140-AAU01174) which are non-antigenic, non-endogenous materials
CC which can be synthetically modified to make them more strongly antigenic,
CC thereby provoking the formation of relatively large quantities of
CC antibodies to the non-endogenous materials in the body of the animals,
CC with consequent reduced risk of damage to the immune system, if exposed
CC to non-endogenous materials.
XX
SQ Sequence 145 AA;

Query Match 80.6%; Score 793; DB 22; Length 145;
Best Local Similarity 100.0%; Pred. No. 7e-56;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
           |||||||||||||||||||||||||
Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145
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Search completed: November 20, 2002, 17:27:36
Job time : 28.8182 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:27 ; Search time 11.965 Seconds
(without alignments)
1422.126 Million cell updates/sec

Title: US-09-787-494-2
Perfect score: 984
Sequence: 1 MTMITDSLAVVLQRRDWENP.....LPGPSDTPILPQTSHHHHHH 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	793	80.6	165	1	KTHUB	choriogonadotropin
2	785	79.8	145	2	I37231	beta-gonadotropin
3	651	66.2	165	1	KTBAB	choriogonadotropin
4	540	54.9	141	1	UTHUB	lutropin beta chai
5	446	45.3	169	1	KTHOB	choriogonadotropin
6	437	44.4	141	1	UTBOB	lutropin beta chai
7	437	44.4	141	1	UTSHB	lutropin beta chai
8	434	44.1	141	1	UTRTB	lutropin beta chai
9	433	44.0	139	2	I52320	testicular luteini
10	427	43.4	119	2	A61465	lutropin beta chai
11	427	43.4	141	1	UTPGB	lutropin beta chai
12	423	43.0	141	2	JC4527	luteinizing hormon
13	420	42.7	138	2	S00512	lutropin beta chai
14	407	41.4	118	2	PN0139	lutropin beta chai
15	406	41.3	118	2	PN0141	lutropin beta chai
16	303	30.8	144	1	UTCAB	gonadotropin beta
17	301	30.6	141	1	B60626	gonadotropin beta
18	301	30.6	146	1	S16763	gonadotropin beta
19	297	30.2	142	2	I51232	gonadotropin II be
20	294	29.9	142	1	C36179	gonadotropin II be
21	280	28.5	142	1	A25800	gonadotropin beta
22	276.5	28.1	113	1	S07092	gonadotropin beta
23	274	27.8	142	2	I50143	gonadotropin II be
24	273	27.7	140	2	A48166	gonadotropin II be
25	269	27.3	128	2	S74085	lutropin beta chai
26	267	27.1	158	2	A61091	lutropin beta chai
27	265	26.9	112	2	S21196	lutropin beta chai
28	258	26.2	166	2	I51242	luteinizing hormon
29	255.5	26.0	80	2	I65235	testicular luteini
30	255	25.9	147	2	I50994	gonadotropin II be
31	255	25.9	159	2	I51373	luteinizing hormon
32	243	24.7	138	1	TTHUB	thyrotropin beta c
33	243	24.7	138	1	TTBOB	thyrotropin beta c
34	242	24.6	138	1	TTPGB	thyrotropin beta c
35	240	24.4	138	2	A29479	thyrotropin beta c
36	239	24.3	138	1	TTRTB	thyrotropin beta c
37	229	23.3	136	2	I50554	gonadotropin II be
38	227	23.1	118	1	FTHOB	follitropin beta c
39	222	22.6	130	2	JC4526	follitropin beta c
40	218	22.2	129	1	FTSHB	follitropin beta c
41	218	22.2	130	2	A32893	follitropin beta c
42	215	21.8	129	1	FTHUB	follitropin beta c
43	212	21.5	129	2	A23550	follitropin beta c
44	208	21.1	129	1	FTPGB	follitropin beta c
45	206	20.9	147	2	S34148	thyrotropin beta c

ALIGNMENTS

RESULT 1
KTHUB
choriogonadotropin beta chain precursor [validated] - human
N;Alternate names: beta-gonadotropin; chorionic gonadotropin beta chain
C;Species: Homo sapiens (man)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 08-Dec-2000
C;Accession: A93230; I69972; I55224; I55250; I70007; I70008; A92303; A92181; A92142;
R;Fiddes, J.C.; Goodman, H.M.
Nature 286, 684-687, 1980
A;Title: The cDNA for the beta-subunit of human chorionic gonadotropin suggests evolu
A;Reference number: A93230; MUID:81012134; PMID:6774259
A;Accession: A93230
A;Molecule type: mRNA
A;Residues: 1-165 <FID>
A;Cross-references: GB:J00117; GB:M38559; GB:M54963; NID:g180436; PIDN:AAA96690.1; PI
R;Policastro, P.; Ovitt, C.E.; Hoshina, M.; Fukuoka, H.; Boothby, M.R.; Boime, I.
J. Biol. Chem. 258, 11492-11499, 1983
A;Title: The beta subunit of human chorionic gonadotropin is encoded by multiple gene
A;Reference number: I55224; MUID:84008141; PMID:6194155
A;Accession: I69972
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-165 <POL>
A;Cross-references: GB:K03189; NID:g180450; PIDN:AAA53288.1; PID:g180453
A;Note: clone CG-beta-e
A;Accession: I55224
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-23,'M',25-136,'A',138-165 <PO2>
A;Cross-references: GB:K03183; NID:g180442; PIDN:AAA53287.1; PID:g180444
A;Note: clone CG-beta-a
R;Policastro, P.F.; Daniels-McQueen, S.; Carle, G.; Boime, I.
J. Biol. Chem. 261, 5907-5916, 1986
A;Title: A map of the hCG beta-LH beta gene cluster.
A;Reference number: I55250; MUID:86195987; PMID:2422163
A;Accession: I55250
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5 <PO3>
A;Cross-references: GB:M13504; NID:g180419; PIDN:AAA52005.1; PID:g463088
A;Note: CG-beta-3 gene
A;Accession: I70007
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5 <PO4>
A;Cross-references: GB:M13505; NID:g180429; PIDN:AAA52008.1; PID:g463089
A;Note: CG-beta-6 gene
A;Accession: I70008
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5 <RE5>
A;Cross-references: GB:M13503; NID:g180432; PIDN:AAA52009.1; PID:g463090

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A;Note: CG-beta-7 gene
R;Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.
J. Biol. Chem. 256, 1816-1823, 1981
A;Title: The amino acid sequences of the prepeptides contained in the alpha and beta sut
A;Reference number: A92303; MUID:81117268; PMID:7462224
A;Accession: A92303
A;Molecule type: protein
A;Residues: 1-20 <BIR>
A;Note: the identity of the residue at position 19 could not be determined
R;Morgan, F.J.; Birken, S.; Canfield, R.E.
J. Biol. Chem. 250, 5247-5258, 1975
A;Title: The amino acid sequence of human chorionic gonadotropin. The alpha subunit and
A;Reference number: A92181; MUID:75211304; PMID:1150658
A;Accession: A92181
A;Molecule type: protein
A;Residues: 21-165 <MOR>
R;Carlsen, R.B.; Bahl, O.P.; Swaminathan, N.
J. Biol. Chem. 248, 6810-6827, 1973
A;Reference number: A92142; MUID:74011267; PMID:4795659
A;Accession: A92142
A;Molecule type: protein
A;Residues: 21-22,'Q',24-73,'ZL',76-140,142-157,'PB',160-165,'SLP' <CAR>
R;Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.; Wang, Y.
Chinese Biochem. J. 6, 558-562, 1990
A;Title: The immunological characteristics of the enzymatic fragments of human chorionic
A;Reference number: PC1016
A;Accession: PC1016
A;Molecule type: protein
A;Residues: 21-165 <SHI>
A;Note: article in Chinese with English abstract
R;Birken, S.; Armstrong, E.G.; Kolks, M.A.G.; Cole, L.A.; Agosto, G.M.; Krichevsky, A.;
Endocrinology 123, 572-583, 1988
A;Title: Structure of the human chorionic gonadotropin beta-subunit fragment from pregna
A;Reference number: A61097; MUID:88254680; PMID:2454811
A;Accession: A61097
A;Molecule type: protein
A;Residues: 26-32,'X',34-49,'X',51-60;75-112 <BI2>
A;Note: this material from pregancy urine lacks sialic acid in its carbohydrate and has
R;Kardana, A.; Bagshawe, K.D.; Coles,' B.; Read, D.; Taylor, M.
Br. J. Cancer 67, 686-692, 1993
A;Title: Characterisation of UGP and its relationship with beta-core fragment.
A;Reference number: A56873; MUID:93229246; PMID:8471426
A;Accession: B56873
A;Molecule type: protein
A;Residues: 26-28,'X',30-32,'X',34-42,'X',44-45,'X',47-48;75-76,'X',78-91,'G',93-102 <KA
A;Experimental source: urine
A;Note: sequence modified after extraction from NCBI backbone
A;Note: this material was designated urinary gonadotrophin peptide (peak 2)
R;Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader, J.W.; Canfield, R.E.; Machin,
Nature 369, 455-461, 1994
A;Title: Crystal structure of human chorionic gonadotropin.
A;Reference number: A44674; MUID:94261179; PMID:8202136
A;Contents: annotation; X-ray crystallography, 3.0 angstroms; correction of disulfide bo
R;Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
Nature 307, 37-40, 1984
A;Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin an
A;Reference number: I37231; MUID:84093590; PMID:6690982
A;Accession: I37412
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 21-165 <RES>
A;Cross-references: EMBL:X00265; NID:g31719; PIDN:CAA25068.1; PID:g1335075
C;Genetics:
A;Gene: GDB:CGB
A;Cross-references: GDB:119055; OMIM:118860
A;Map position: 19q13.3-19q13.3
A;Introns: 5/3; 61/3
A;Note: the choriogonadotropin beta chain locus contains six genes (or pseudogenes)
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: glycoprotein; hormone; pituitary
F;1-20/Domain: signal sequence #status experimental <SIG>
F;21-165/Product: choriogonadotropin beta chain #status experimental <MAT>
F;29-77,43-92,46-130,54-108,58-110,113-120/Disulfide bonds: #status experimental
F;33,50/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;138,150/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;141,147,152,158/Binding site: carbohydrate (Ser) (covalent) #status experimental

  Query Match             80.6%;  Score 793;  DB 1;  Length 165;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-56;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
           |||||||||||||||||||||||||
Db     142 KAPPPSLPSPSRLPGPSDTPILPQ 165


RESULT 2
I37231
beta-gonadotropin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jul-2000
C;Accession: I37231
R;Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
Nature 307, 37-40, 1984
A;Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin
A;Reference number: I37231; MUID:84093590; PMID:6690982
A;Accession: I37231
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-145 <RES>
A;Cross-references: EMBL:X00266; NID:g29907; PIDN:CAA25069.1; PID:g1335012
C;Genetics:
A;Introns: 41/3
C;Superfamily: pituitary glycoprotein hormone beta chain

  Query Match             79.8%;  Score 785;  DB 2;  Length 145;
  Best Local Similarity   99.3%;  Pred. No. 2.1e-55;
  Matches  143;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQASSSS 121

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
           |||||||||||||||||||||||||
Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 3
KTBAB
choriogonadotropin beta chain precursor - olive baboon
C;Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 28-May-1999
C;Accession: A25808
R;Crawford, R.J.; Tregear, G.W.; Niall, H.D.
Gene 46, 161-169, 1986
A;Title: The nucleotide sequences of baboon chorionic gonadotropin beta-subunit genes
A;Reference number: A25808; MUID:87106851; PMID:2433190
A;Accession: A25808
A;Molecule type: mRNA
A;Residues: 1-165 <CRA>
A;Cross-references: GB:M14966; NID:g176572; PIDN:AAA35383.1; PID:g176573
C;Comment: There are at least five copies of CG-related genes and at least two of the
C;Superfamily: pituitary glycoprotein hormone beta chain
```

C;Keywords: glycoprotein; hormone; placenta; pregnancy maintenance
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-165/Product: choriogonadotropin beta chain #status predicted <CGB>
F;29-77,43-92,46-130,54-108,58-110,113-120/Disulfide bonds: #status predicted
F;33,50/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;140,147,152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 66.2%; Score 651; DB 1; Length 165;
Best Local Similarity 79.2%; Pred. No. 9.7e-45;
Matches 118; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

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Qy      21 GCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVV 80
           | :  :||||| |||||||||| ||| ||||:||||||||||||||| |||| ||| :||||
Db      17 GAQASREPLRPLCRPINATLAAEKEACPVCVTVNTTICAGYCPTMMRVLQAVLPPVPQVV 76

Qy      81 CNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQ 140
           ||||:||||||||||||| ||:|:||  |||||:||||||||:|||||||||||||||  |
Db      77 CNYREVRFESIRLPGCPPGVDPMVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPNLQ 136

Qy     141 DSSSSKAPPPSLPSPSRLPGPSDTPILPQ 169
           ||||| |||| |||||| |: || |||
Db     137 ASSSSKDPPPSPPSPSRLLEPAGTPFLPQ 165
```

RESULT 4
UTHUB
lutropin beta chain precursor [validated] - human
N;Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
C;Species: Homo sapiens (man)
C;Date: 13-Jul-1981 #sequence_revision 24-Nov-1999 #text_change 20-Apr-2001
C;Accession: I37994; I58013; A90604; A92759; A94466; A01497; B94552
R;Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
Nature 307, 37-40, 1984
A;Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin an
A;Reference number: I37231; MUID:84093590; PMID:6690982
A;Accession: I37994
A;Status: preliminary; translated from GB/EMBL/DDBJ; not compared with conceptual transl
A;Molecule type: DNA
A;Residues: 1-141 <TAL>
A;Cross-references: GB:X00264; NID:g34351; PIDN:CAA25067.1; PID:g2292893
R;Weiss, J.; Axelrod, L.; Whitcomb, R.W.; Harris, P.E.; Crowley, W.F.; Jameson, J.L.
N. Engl. J. Med. 326, 179-183, 1992
A;Title: Hypogonadism caused by a single amino acid substitution in the beta subunit of
A;Reference number: I58013; MUID:92085985; PMID:1727547
A;Accession: I58013
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 72-73,'R',75-76 <WEI>
A;Cross-references: GB:S71273; NID:g240572; PIDN:AAD14960.1; PID:g4262812
A;Note: mutant sequence from patient with hypogonadism
R;Sairam, M.R.; Li, C.H.
Biochim. Biophys. Acta 412, 70-81, 1975
A;Title: Human pituitary lutropin. Isolation, properties, and the complete amino acid se
A;Reference number: A90604; MUID:76062547; PMID:1191677
A;Accession: A90604
A;Molecule type: protein
A;Residues: 21-38,'Q',40-75,77-131,133-134,'H',136-137 <SAI>
R;Shome, B.; Parlow, A.F.
J. Clin. Endocrinol. Metab. 36, 618-621, 1973
A;Title: The primary structure of the hormone-specific, beta subunit of human pituitary
A;Reference number: A92759; MUID:73090987; PMID:4685398
A;Accession: A92759
A;Molecule type: protein
A;Residues: 21-38,'Q',40-75,77-131,133-134,'H',136-137 <SHO>
R;Closset, J.; Hennen, G.; Lequin, R.M.
FEBS Lett. 29, 97-100, 1973
A;Title: Human luteinizing hormone the amino acid sequence of the beta subunit.
A;Reference number: A91389; MUID:73221227; PMID:4719207
A;Contents: annotation; partial sequence
R;Ward, D.N.
unpublished results, cited by Closset, J., Hennen, G., and Lequin, R.M., FEBS Lett. 29,
A;Reference number: A94466
A;Accession: A94466
A;Molecule type: protein
A;Residues: 21-38,'Q',40-46 <WAR>
A;Note: 28-Val, 33-Arg, and 35-Thr were also found
R;Shome, B.; Parlow, A.F.
submitted to the Atlas, April 1975
A;Reference number: A94552
A;Contents: annotation; binding site
C;Genetics:
A;Gene: GDB:LHB
A;Cross-references: GDB:119364; OMIM:152780
A;Map position: 19q13.3-19q13.3
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: blocked amino end; glycoprotein; hormone; pituitary
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-141/Product: lutropin beta #status experimental <LTB>
F;21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #s
F;29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F;50/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 54.9%; Score 540; DB 1; Length 141;
Best Local Similarity 85.0%; Pred. No. 5.1e-36;
Matches 96; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

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Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           :||||| | |||| |||||||||||||||||||||||| |||| ||| |||||| |||
Db      22 REPLRPWCHPINAILAVEKEGCPVCITVNTTICAGYCPTMMRVLQAVLPPLPQVVCTYRD 81

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPR 138
           ||||||||||||||:||||: |||||:|  |||||:|||||||||||||| |:
Db      82 VRFESIRLPGCPRGVDPVVSFPVALSCRCGPCRRSTSDCGGPKDHPLTCDHPQ 134
```

RESULT 5
KTHOB
choriogonadotropin beta chain precursor - horse
N;Alternate names: chorionic gonadotropin beta chain (CG); luteinizing hormone (LH) b
C;Species: Equus caballus (domestic horse)
C;Date: 14-Nov-1983 #sequence_revision 03-May-1996 #text_change 18-Jun-1999
C;Accession: A41917; A29304; A29305; A01503
R;Sherman, G.B.; Wolfe, M.W.; Farmerie, T.A.; Clay, C.M.; Threadgill, D.S.; Sharp, D.
Mol. Endocrinol. 6, 951-959, 1992
A;Title: A single gene encodes the beta-subunits of equine luteinizing hormone and ch
A;Reference number: A41917; MUID:92357035; PMID:1379674
A;Accession: A41917
A;Molecule type: DNA
A;Residues: 1-169 <SHE>
A;Cross-references: GB:S41704; NID:g252740; PIDN:AAB22775.1; PID:g252741
A;Experimental source: sperm
A;Note: sequence extracted from NCBI backbone (NCBIN:110184, NCBIP:110185)
R;Sugino, H.; Bousfield, G.R.; Moore Jr., W.T.; Ward, D.N.
J. Biol. Chem. 262, 8603-8609, 1987
A;Title: Structural studies on equine glycoprotein hormones. Amino acid sequence of e
A;Reference number: A29304; MUID:87250475; PMID:3298238
A;Accession: A29304
A;Molecule type: protein
A;Residues: 21-169 <SUG>
R;Bousfield, G.R.; Liu, W.K.; Sugino, H.; Ward, D.N.
J. Biol. Chem. 262, 8610-8620, 1987
A;Title: Structural studies on equine glycoprotein hormones. Amino acid sequence of e
A;Reference number: A29305; MUID:87250476; PMID:3298239
A;Accession: A29305
A;Molecule type: protein
A;Residues: 21-169 <BOU>
R;Ward, D.N.; Moore Jr., W.T.; Burleigh, B.D.
J. Protein Chem. 1, 263-280, 1982
A;Title: Structural studies on equine chorionic gonadotropin.
A;Reference number: A01503
A;Accession: A01503
A;Molecule type: protein
A;Residues: 21-40,'Q',42-43,'SK',46,'XXXX',51,'T',53-64,'T',66-96,'B',98,'R',100-102,
R;Matsui, T.; Mizuochi, T.; Titani, K.; Okinaga, T.; Hoshi, M.; Bousfield, G.R.; Sugi
Biochemistry 33, 14039-14048, 1994
A;Title: Structural analysis of N-linked oligosaccharides of equine chorionic gonadot

```
A;Reference number: A55952; MUID:95034847; PMID:7524670
A;Contents: annotation; glycosylation
A;Note: horse lutropin and choriogonadotropin beta chains have identical protein chains
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: glycoprotein; hormone; pituitary
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-169/Product: choriogonadotropin beta chain #status experimental <MAT>
F;29-77,43-92,46-130,54-108,58-110,113-120/Disulfide bonds: #status predicted
F;33/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             45.3%;  Score 446;  DB 1;  Length 169;
  Best Local Similarity   55.0%;  Pred. No. 1.7e-28;
  Matches   88;  Conservative   17;  Mismatches   41;  Indels   14;  Gaps    3;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| |||||||| ||| ||:||| |:||||||:| ||:   |||:
Db      19 WASRG------PLRPLCRPINATLAAEKEACPICITFTTSICAGYCPSMVRVMPAALPAI 72

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
           || || ||::|| |||||||| ||:|:||: ||||| |  |:  |||||  :| || |
Db      73 PQPVCTYRELRFASIRLPGCPPGVDPMVSFPVALSCHCGPCQIKTTDCGVFRDQPLACAP 132

Qy     137 PRFQDSSSSKAPPPSLPSPSRLPGP-----SDTPILPQTS 171
             | ||||| ||    : :  | |     |  |:  :||
Db     133 ---QASSSSKDPPSQPLTSTSTPTPGASRRSSHPLPIKTS 169


RESULT 6
UTBOB
lutropin beta chain precursor - bovine
N;Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 24-Nov-1999
C;Accession: A92534; A92518; A91212; A01499
R;Virgin, J.B.; Silver, B.J.; Thomason, A.R.; Nilson, J.H.
J. Biol. Chem. 260, 7072-7077, 1985
A;Title: The gene for the beta subunit of bovine luteinizing hormone encodes a gonadotrc
A;Reference number: A92534; MUID:85207729; PMID:2987241
A;Accession: A92534
A;Molecule type: DNA
A;Residues: 1-141 <VIR>
A;Cross-references: GB:M11506; NID:g163298; PIDN:AAB59267.1; PID:g163299
R;Maurer, R.A.
J. Biol. Chem. 260, 4684-4687, 1985
A;Title: Analysis of several bovine lutropin beta subunit cDNAs reveals heterogeneity ir
A;Reference number: A92518; MUID:85182575; PMID:3838746
A;Accession: A92518
A;Molecule type: mRNA
A;Residues: 3-111,'S',113-141 <MAU>
A;Cross-references: GB:M10077; NID:g163300; PIDN:AAA30623.1; PID:g163301
R;Maghuin-Rogister, G.; Hennen, G.
Eur. J. Biochem. 39, 235-253, 1973
A;Title: Luteinizing hormone. The primary structures of the beta-subunit from bovine and
A;Reference number: A91212; MUID:74075724; PMID:4770795
A;Accession: A91212
A;Molecule type: protein
A;Residues: 21-73,'E',75-121,'PG',124-125,'E',127-139 <MAG>
A;Note: some carboxyl-terminal heterogeneity was found
C;Genetics:
A;Introns: 5/3; 61/3
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: blocked amino end; glycoprotein; hormone; pituitary
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-141/Product: lutropin beta #status experimental <LTB>
F;21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #stat
F;29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F;33/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             44.4%;  Score 437;  DB 1;  Length 141;
  Best Local Similarity   61.6%;  Pred. No. 7.3e-28;
  Matches   77;  Conservative   14;  Mismatches   28;  Indels    6;  Gaps    1;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| |:||||||| ||| ||||||  |:|||||||:| |||  :|| :
Db      19 WASRG------PLRPLCQPINATLAAEKEACPVCITFTTSICAGYCPSMKRVLPVILPPM 72

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
           || || | ::|| |:|||||| ||:|:||: ||||| |  || |:|||||:  || ||
Db      73 PQRVCTYHELRFASVRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDH 132

Qy     137 PRFQD 141
           |   |
Db     133 PPLPD 137


RESULT 7
UTSHB
lutropin beta chain precursor - sheep
N;Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizi
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 24-Apr-1984 #sequence_revision 19-Jan-2001 #text_change 19-Jan-2001
C;Accession: I46949; S09232; A92110; A90053; B61098; A01500
R;Brown, P.; McNeilly, J.R.; Wallace, R.M.; McNeilly, A.S.; Clark, A.J.
Mol. Cell. Endocrinol. 93, 157-165, 1993
A;Title: Characterization of the ovine LH beta-subunit gene: the promoter directs gon
A;Reference number: I46949; MUID:93351742; PMID:8349025
A;Accession: I46949
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-141 <BRO>
A;Cross-references: GB:S64695; NID:g408240; PIDN:AAB27819.1; PID:g408241
R;d'Angelo-Bernard, G.; Moumni, M.; Jutisz, M.; Counis, R.
Nucleic Acids Res. 18, 2175, 1990
A;Title: Cloning and sequence analysis of the cDNA for the precursor of the beta subu
A;Reference number: S09232; MUID:90245669; PMID:2336396
A;Accession: S09232
A;Molecule type: mRNA
A;Residues: 1-58,'L',60-62,'Q',64-141 <ANG>
A;Cross-references: EMBL:X52488; NID:g1319; PIDN:CAA36729.1; PID:g1320
R;Liu, W.K.; Nahm, H.S.; Sweeney, C.M.; Holcomb, G.N.; Ward, D.N.
J. Biol. Chem. 247, 4365-4381, 1972
A;Title: The primary structure of ovine luteinizing hormone. II. The amino acid seque
A;Reference number: A92110; MUID:72211145; PMID:4556309
A;Accession: A92110
A;Molecule type: protein
A;Residues: 21-121,'PG',124-125,'E',127-139 <LIU>
R;Sairam, M.R.; Samy, T.S.A.; Papkoff, H.; Li, C.H.
Arch. Biochem. Biophys. 153, 572-586, 1972
A;Title: The primary structure of ovine interstitial cell-stimulating hormone. II. Th
A;Reference number: A90053; MUID:73190035; PMID:4575435
A;Accession: A90053
A;Molecule type: protein
A;Residues: 21-29,'E',31-71,'P',72-80,'Q',82-121,'PG',124-125,'E',127-139 <SAI>
R;Nomura, K.; Tsunasawa, S.; Ohmura, K.; Sakiyama, F.; Shizume, K.
Endocrinology 123, 700-712, 1988
A;Title: Renotropic activity in ovine luteinizing hormone isoform(s).
A;Reference number: A61098; MUID:88283534; PMID:2456202
A;Accession: B61098
A;Molecule type: protein
A;Residues: 21-39,'N',41-49;64-78,'V',80-82;84-106;115-121,'PG',124-138 <NOM>
A;Note: this form was designated form beta-3; forms beta-1 and beta-2 each lack sever
C;Genetics:
A;Introns: 5/3; 61/3
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: blocked amino end; glycoprotein; hormone; pituitary
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-141/Product: lutropin beta chain #status experimental <MAT>
F;21/Modified site: blocked amino end (Ser) (in mature form) (partial) (probably acet
F;29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F;33/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             44.4%;  Score 437;  DB 1;  Length 141;
  Best Local Similarity   61.6%;  Pred. No. 7.3e-28;
  Matches   77;  Conservative   14;  Mismatches   28;  Indels    6;  Gaps    1;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
```

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          | : |      |||| |:|||||||| ||| ||||||  |:|||||||:| |||  :|| :
Db      19 WASRG------PLRPLCQPINATLAAEKEACPVCITFTTSICAGYCPSMKRVLPVILPPM 72

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
           || || | ::|| |:|||||| ||:|:||: ||||| |  || |:||||||:  || ||
Db      73 PQRVCTYHELRFASVRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDH 132

Qy     137 PRFQD 141
           |   |
Db     133 PPLPD 137


RESULT 8
UTRTB
lutropin beta chain precursor - rat
N;Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 24-Sep-1999
C;Accession: A01498; PQ0091; S42527; I83049
R;Jameson, L.; Chin, W.W.; Hollenberg, A.N.; Chang, A.S.; Habener, J.F.
J. Biol. Chem. 259, 15474-15480, 1984
A;Title: The gene encoding the beta-subunit of rat lutenizing hormone. Analysis of gene
A;Reference number: A01498; MUID:85080043; PMID:6096374
A;Accession: A01498
A;Molecule type: DNA
A;Residues: 1-141 <JAM>
A;Cross-references: EMBL:J00749; NID:g205175; PIDN:AAA96703.1; PID:g205176
R;Kato, Y.; Ezashi, T.; Hirai, T.; Kato, T.
submitted to JIPID, July 1990
A;Reference number: PQ0091
A;Accession: PQ0091
A;Molecule type: mRNA
A;Residues: 4-141 <KAT>
R;Chin, W.W.; Godine, J.E.; Klein, D.R.; Chang, A.S.; Tan, L.K.; Habener, J.F.
Proc. Natl. Acad. Sci. U.S.A. 80, 4649-4653, 1983
A;Title: Nucleotide sequence of the cDNA encoding the precursor of the beta subunit of r
A;Reference number: S42527; MUID:83273673; PMID:6192440
A;Accession: S42527
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-141 <CHI>
A;Cross-references: GB:J00749; GB:M54957; NID:g205175; PIDN:AAA96703.1; PID:g205176
R;Kato, Y.; Ezashi, T.; Hirai, T.; Kato, T.
Zool. Sci. 7, 879-887, 1990
A;Title: Strain Difference in Nucleotide Sequences of Rat Glycoprotein Hormone Subunit c
A;Reference number: I60104
A;Accession: I83049
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 4-141 <RES>
A;Cross-references: GB:D00576; NID:g220807; PIDN:BAA00454.1; PID:g220808
C;Comment: The beta chain confers the specificity of the hormone.
C;Genetics:
A;Introns: 5/3; 61/3
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: glycoprotein; hormone; pituitary
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-141/Product: lutropin beta #status predicted <LTB>
F;29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F;33/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             44.1%;  Score 434;  DB 1;  Length 141;
  Best Local Similarity   62.0%;  Pred. No. 1.3e-27;
  Matches   75;  Conservative   16;  Mismatches   24;  Indels    6;  Gaps    1;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| |||:||||| | | ||||||  |:|||||||:| |||   || :
Db      19 WASRG------PLRPLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPV 72

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
           || || ||::|| |:|||||| ||:|:||: |||||:|  || |::|||||:  || ||
Db      73 PQPVCTYRELRFASVRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMTCDL 132

Qy     137 P 137
           |
Db     133 P 133


RESULT 9
I52320
testicular luteinizing hormone beta-subunit - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C;Accession: I52320
R;Zhang, F.P.; Rannikko, A.; Huhtaniemi, I.
Biochem. Biophys. Res. Commun. 210, 858-865, 1995
A;Title: Isolation and characterization of testis-specific cDNAs for luteinizing horm
A;Reference number: I52320; MUID:95283549; PMID:7763258
A;Accession: I52320
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-139 <RES>
A;Cross-references: EMBL:U25653; NID:g915216; PIDN:AAC52249.1; PID:g915217
C;Genetics:
A;Gene: TLHB1
C;Superfamily: pituitary glycoprotein hormone beta chain

  Query Match             44.0%;  Score 433;  DB 2;  Length 139;
  Best Local Similarity   61.2%;  Pred. No. 1.5e-27;
  Matches   74;  Conservative   17;  Mismatches   24;  Indels    6;  Gaps    1;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| |||:||||| | | ||||||  |:|||||||:| |:|   || :
Db      17 WASRG------PLRPLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRILPAALPPV 70

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
           || || ||::|| |:|||||| ||:|:||: |||||:|  || |::|||||:  |:|||
Db      71 PQPVCTYRELRFASVRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMTCDL 130

Qy     137 P 137
           |
Db     131 P 131


RESULT 10
A61465
lutropin beta chain - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 08-Dec-1995
C;Accession: A61465
R;Glenn, S.D.; Nahm, H.S.; Ward, D.N.
J. Protein Chem. 3, 259-273, 1984
A;Title: The amino acid sequence of the rabbit lutropin beta subunit.
A;Reference number: A61465
A;Accession: A61465
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-119 <GLE>
A;Note: the sequence from Fig. 1 is inconsistent with that from the abstract in havin
C;Superfamily: pituitary glycoprotein hormone beta chain
F;11-36,25-59,28-90,40-112,74-102,92-95/Disulfide bonds: #status predicted

  Query Match             43.4%;  Score 427;  DB 2;  Length 119;
  Best Local Similarity   67.3%;  Pred. No. 3.8e-27;
  Matches   74;  Conservative   12;  Mismatches   24;  Indels    0;  Gaps    0;

Qy      28 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 87
           |||| |||:||||| | | ||||||  |:|||||||:| |||   || :|| || ||::|
Db       6 PLRPLCRPVNATLAAENEACPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELR 65

Qy      88 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 137
           | |||||||| ||:| ||: |||||:|  || |::|||||:  || || |
Db      66 FASIRLPGCPPGVDPEVSFPVALSCRCGPCRLSSSDCGGPRAEPLACDLP 115


RESULT 11
```

```
UTPGB
lutropin beta chain precursor - pig
N;Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 30-Jun-1993 #text_change 16-Jun-2000
C;Accession: A48170; A30322; A01501; A60584
R;Ezashi, T.; Hirai, T.; Kato, T.; Wakabayashi, K.; Kato, Y.
J. Mol. Endocrinol. 5, 137-146, 1990
A;Title: The gene for the beta subunit of porcine LH: clusters of GC boxes and CACCC ele
A;Reference number: A48170; MUID:91063934; PMID:1701088
A;Accession: A48170
A;Molecule type: DNA
A;Residues: 1-141 <EZA>
A;Cross-references: GB:D00579; NID:g217693; PIDN:BAA00457.1; PID:g217694
R;Kato, Y.; Hirai, T.
Mol. Cell. Endocrinol. 62, 47-53, 1989
A;Title: Cloning and DNA sequence analysis of the cDNA for the precursor of porcine lute
A;Reference number: A30322; MUID:89306142; PMID:2744222
A;Accession: A30322
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-141 <KAT>
R;Maghuin-Rogister, G.; Hennen, G.
Eur. J. Biochem. 39, 235-253, 1973
A;Title: Luteinizing hormone. The primary structures of the beta-subunit from bovine and
A;Reference number: A91212; MUID:74075724; PMID:4770795
A;Accession: A01501
A;Molecule type: protein
A;Residues: 21-29,'Z',31-39,'D',41-61,'R',63-82,'I',84-86,'S',88-121,'PG',124-133,'P',13
A;Note: 30-Arg was also found
A;Note: about half the chains lack one or both carboxyl-terminal leucines
R;Nomura, K.; Ohmura, K.; Nakamura, Y.; Horiba, N.; Shirakura, Y.; Sato, Y.; Ujihara, M.
Endocrinology 124, 712-719, 1989
A;Title: Porcine luteinizing hormone isoform(s): relationship between their molecular st
A;Reference number: A60584; MUID:89107050; PMID:2536317
A;Accession: A60584
A;Molecule type: protein
A;Residues: 21-31;137-139 <NOM>
A;Note: the lutropin beta chain is heterogeneous at the carboxyl end; this form lacked t
C;Genetics:
A;Introns: 5/3; 61/3
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: blocked amino end; glycoprotein; hormone
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-141/Product: lutropin beta chain #status experimental <MAT>
F;21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #stat
F;29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F;33/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             43.4%;  Score 427;  DB 1;  Length 141;
  Best Local Similarity   62.8%;  Pred. No. 4.5e-27;
  Matches   76;  Conservative   11;  Mismatches   28;  Indels    6;  Gaps    1;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| |||||||||| | | ||||||  |:|||||||:| |||   || :
Db      19 WASRG------PLRPLCRPINATLAAENEACPVCITFTTSICAGYCPSMVRVLPAALPPV 72

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
           || || ||:: | |||||||| ||:| ||: ||||| |  || |::|||||:  || ||
Db      73 PQPVCTYRELSFASIRLPGCPPGVDPTVSFPVALSCHCGPCRLSSSDCGGPRAQPLACDR 132

Qy     137 P 137
           |
Db     133 P 133


RESULT 12
JC4527
luteinizing hormone beta chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 16-Jul-1999
C;Accession: JC4527
R;Kumar, T.R.; Matzuk, M.M.
Gene 166, 335-336, 1995
A;Title: Cloning of the mouse gonadotropin beta-subunit-encoding genes, II. Structur
A;Reference number: JC4527; MUID:96125216; PMID:8543188
A;Accession: JC4527
A;Molecule type: mRNA
A;Residues: 1-141 <KUM>
A;Cross-references: GB:U25145; NID:g930344; PIDN:AAA92841.1; PID:g930345
A;Experimental source: 129SvEv
C;Comment: This protein is co-produced with follicle-stimulating hormone in pituitar
n reproduction including gonadal growth, gametogenesis and steroidogenesis.
C;Genetics:
A;Gene: lh beta
A;Introns: 5/3; 61/3
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: hormone; reproduction
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-141/Product: luteinizing hormone beta chain #status predicted <MAT>

  Query Match             43.0%;  Score 423;  DB 2;  Length 141;
  Best Local Similarity   60.3%;  Pred. No. 9.3e-27;
  Matches   73;  Conservative   16;  Mismatches   26;  Indels    6;  Gaps    1;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| |||:||||| | | ||||||  |:||||||||:| |||   || :
Db      19 WASRG------PLRPLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPV 72

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
           || || ||:: | |:|||||| ||:|:||: |||||:|  || |::||||:  |: ||
Db      73 PQPVCTYRELAFASVRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMACDL 132

Qy     137 P 137
           |
Db     133 P 133


RESULT 13
S00512
lutropin beta chain precursor - dog (fragment)
N;Alternate names: luteinizing hormone beta chain
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Accession: S00512
R;Wolf, D.L.; Appleby, V.L.; Hjerrild, K.; Baker, A.R.; Talmadge, K.
Nucleic Acids Res. 15, 10602, 1987
A;Title: Nucleic acid and amino acid sequences of dog beta-LH: comparison to rat, cow
A;Reference number: S00512; MUID:88096605; PMID:3697104
A;Accession: S00512
A;Molecule type: mRNA
A;Residues: 1-138 <WOL>
A;Cross-references: EMBL:Y00518; NID:g907; PIDN:CAA68572.1; PID:g860906
C;Superfamily: pituitary glycoprotein hormone beta chain
F;1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F;18-138/Product: lutropin beta chain #status predicted <MAT>
F;26-51,40-74,43-105,55-127,89-117,107-110/Disulfide bonds: #status predicted

  Query Match             42.7%;  Score 420;  DB 2;  Length 138;
  Best Local Similarity   62.0%;  Pred. No. 1.6e-26;
  Matches   75;  Conservative   11;  Mismatches   29;  Indels    6;  Gaps    1;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| |||||||||| | | ||||||  ||||||||:| |||   || :
Db      16 WASRG------PLRPLCRPINATLAAENEACPVCITFTTTICAGYCPSMVRVLPAALPPV 69

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
           || || | :: | |||||||| ||:|:||: |||||:|  || | :|||||:   | ||
Db      70 PQPVCTYHELHFASIRLPGCPPGVDPMVSFPVALSCRCGPCRLSNSDCGGPRAQSLACDR 129

Qy     137 P 137
           |
Db     130 P 130


RESULT 14
```

```
PN0139
lutropin beta chain - minke whale
N;Alternate names: luteinizing hormone beta chain
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 08-Dec-1995
C;Accession: PN0139
R;Karasev, V.S.; Pankov, Y.A.
Biokhimiia 50, 1972-1986, 1985
A;Title: Amino acid sequence of reduced and carboxymethylated alpha- and beta-subunits c
A;Reference number: PN0138
A;Accession: PN0139
A;Molecule type: protein
A;Residues: 1-118 <KAR>
A;Note: article in Russian with English abstract
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: glycoprotein; hormone
F;9-34,23-57,26-88,38-110,72-100,90-93/Disulfide bonds: #status predicted
F;13/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             41.4%;  Score 407;  DB 2;  Length 118;
  Best Local Similarity   56.0%;  Pred. No. 1.5e-25;
  Matches   70;  Conservative   18;  Mismatches   27;  Indels   10;  Gaps    1;

Qy      28 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 87
           |||| ||||||||| : : ||||||  |:||||||:| |||   || :|: || ||::|
Db       4 PLRPLCRPINATLAAAZBZACPVCITFTTSICAGYCPSMVRVLPAALPPVPZPVCTYRZLR 63

Qy      88 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKA 147
           | |||||||| ||:|:||: ||||| |  || |:::||  :  || |:          ::
Db      64 FASIRLPGCPPGVBPMVSFPVALSCHCGPCRLSSSBCGPGRAZPLACB----------RS 113

Qy     148 PPPSL 152
           | | |
Db     114 PRPGL 118


RESULT 15
PN0141
lutropin beta chain - sperm whale
N;Alternate names: luteinizing hormone beta chain
C;Species: Physeter catodon (sperm whale)
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 07-May-1999
C;Accession: PN0141
R;Pankov, Y.A.; Karasev, V.S.
Biokhimiia 49, 1004-1018, 1984
A;Title: Luteinizing hormone of the sperm-whale: amino acid sequence of reduced and carb
A;Reference number: PN0141; MUID:84281133; PMID:6466737
A;Accession: PN0141
A;Molecule type: protein
A;Residues: 1-118 <PAN>
A;Note: article in Russian with English abstract
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: glycoprotein; hormone
F;9-34,23-57,26-88,38-110,72-100,90-93/Disulfide bonds: #status predicted
F;13/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             41.3%;  Score 406;  DB 2;  Length 118;
  Best Local Similarity   57.6%;  Pred. No. 1.7e-25;
  Matches   72;  Conservative   15;  Mismatches   28;  Indels   10;  Gaps    1;

Qy      28 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 87
           |||| ||||||||| : : ||||||  |:||||||:| |||   || :|: || || :|
Db       4 PLRPLCRPINATLAAQNZACPVCITFTTSICAGYCPSMVRVLPAALPPVPZPVCTYRQLR 63

Qy      88 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKA 147
           | |||||||| ||||:||: ||||| |  || |::||  :  || |          :::
Db      64 FASIRLPGCPPGVNPMVSFPVALSCHCGPCRLSSSDCGPGRAQPLAC----------NRS 113

Qy     148 PPPSL 152
           | | |
Db     114 PRPGL 118
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Search completed: November 20, 2002, 17:30:07
Job time : 11.965 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:26 ; Search time 7.01399 Seconds
(without alignments)
1046.667 Million cell updates/sec

Title: US-09-787-494-2
Perfect score: 984
Sequence: 1 MTMITDSLAVVLQRRDWENP.....LPGPSDTPILPQTSHHHHHH 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	793	80.6	165	1	CGHB_HUMAN	P01233 homo sapien
2	651	66.2	165	1	CGHB_PAPAN	P07434 papio anubi
3	540	54.9	141	1	LSHB_HUMAN	P01229 homo sapien
4	516.5	52.5	164	1	CGHB_CALJA	P51500 callithrix
5	476	48.4	169	1	LSHB_EQUBU	O46641 equus burch
6	461	46.8	169	1	LSHB_EQUAS	P19794 equus asinu
7	446	45.3	169	1	LSHB_HORSE	P08751 equus cabal
8	444	45.1	143	1	LSHB_FELCA	O77805 felis silve
9	437	44.4	141	1	LSHB_BOVIN	P04651 bos taurus
10	434	44.1	141	1	LSHB_RAT	P01230 rattus norv
11	428	43.5	141	1	LSHB_CERSI	O77835 ceratotheri
12	427	43.4	141	1	LSHB_PIG	P01232 sus scrofa
13	427	43.4	141	1	LSHB_SHEEP	P01231 ovis aries
14	423	43.0	141	1	LSHB_MOUSE	O09108 mus musculu
15	420	42.7	138	1	LSHB_CANFA	P18842 canis famil
16	407	41.4	118	1	LSHB_BALAC	P33088 balaenopter
17	407	41.4	128	1	LSHB_PHOSU	Q9qya9 phodopus su
18	406	41.3	118	1	LSHB_PHYCA	P25330 physeter ca
19	405.5	41.2	138	1	LSHB_MACRU	O46483 macropus ru
20	393	39.9	141	1	LSHB_TRIVU	O46482 trichosurus
21	303	30.8	140	1	GTH2_CARAU	Q98849 carassius a
22	303	30.8	144	1	GTH2_CYPCA	P01235 cyprinus ca
23	301	30.6	141	1	GTH2_HYPMO	P37038 hypophthalm
24	301	30.6	146	1	GTH2_CTEID	P30984 ctenopharyn
25	297	30.2	142	1	GTH2_ONCMA	P48253 oncorhynchu
26	294	29.9	142	1	GTH2_ONCKE	P10256 oncorhynchu
27	284	28.9	140	1	GTH2_ICTPU	Q9dg80 ictalurus p
28	283	28.8	138	1	GTH2_CLAGA	P53543 clarias gar
29	282	28.7	149	1	GTH2_CLUPA	Q9ygh2 clupea pall
30	280	28.5	142	1	GTH2_ONCTS	P07732 oncorhynchu
31	276.5	28.1	113	1	GTHB_MURCI	P12837 muraenesox
32	274	27.8	142	1	GTH2_CORAU	P48251 coregonus a
33	273	27.7	140	1	GTH2_ANGAN	P27767 anguilla an
34	269	27.3	128	1	LSHB_STRCA	P80664 struthio ca
35	265	26.9	112	1	LSHB_RANCA	P80071 rana catesb
36	258	26.2	166	1	LSHB_COTJA	P45657 coturnix co
37	257	26.1	137	1	GTH2_ACALA	Q90225 acanthopagr
38	255.5	26.0	132	1	GTH1_ICTPU	Q9dg81 ictalurus p
39	255	25.9	139	1	GTH2_MORSA	Q91121 morone saxa
40	255	25.9	146	1	GTH2_TRITC	Q9pw98 trichogaste
41	255	25.9	159	1	LSHB_MELGA	P45646 meleagris g
42	254	25.8	127	1	GTH1_ANGJA	Q9ygk3 anguilla ja
43	254	25.8	138	1	TSHB_CANFA	P54828 canis famil
44	252	25.6	115	1	GTH2_THUOB	P37206 thunnus obe
45	243	24.7	138	1	TSHB_BOVIN	P01223 bos taurus

ALIGNMENTS

RESULT 1
CGHB_HUMAN
ID CGHB_HUMAN STANDARD; PRT; 165 AA.
AC P01233; Q14000; Q13991;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Choriogonadotropin beta chain precursor (Chorionic gonadotrophin beta
DE subunit) (CG-beta).
GN CGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012134; PubMed=6774259;
RA Fiddes J.C., Goodman H.M.;
RT "The cDNA for the beta-subunit of human chorionic gonadotropin
RT suggests evolution of a gene by readthrough into the 3'-untranslated
RT region.";
RL Nature 286:684-687(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84093590; PubMed=6690982;
RA Talmadge K., Vamvakopoulos N.C., Fiddes J.C.;
RT "Evolution of the genes for the beta subunits of human chorionic
RT gonadotropin and luteinizing hormone.";
RL Nature 307:37-40(1984).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=84008141; PubMed=6194155;
RA Policastro P., Ovitt C.E., Hoshina M., Fukuoka H., Boothby M.R.,
RA Boime I.;
RT "The beta subunit of human chorionic gonadotropin is encoded by
RT multiple genes.";
RL J. Biol. Chem. 258:11492-11499(1983).
RN [4]
RP SEQUENCE OF 1-20.
RX MEDLINE=81117268; PubMed=7462224;
RA Birken S., Fetherston J., Canfield R.E., Boime I.;
RT "The amino acid sequences of the prepeptides contained in the alpha
RT and beta subunits of human choriogonadotropin.";
RL J. Biol. Chem. 256:1816-1823(1981).
RN [5]
RP SEQUENCE OF 21-165.
RX MEDLINE=75211304; PubMed=1150658;
RA Morgan F.J., Birken S., Canfield R.E.;
RT "The amino acid sequence of human chorionic gonadotropin. The alpha
RT subunit and beta subunit.";
RL J. Biol. Chem. 250:5247-5258(1975).
RN [6]
RP PRELIMINARY SEQUENCE OF 21-165.
RX MEDLINE=74011267; PubMed=4795659;
RA Carlsen R.B., Bahl O.P., Swaminathan N.;
RT "Human chorionic gonadotropin. Linear amino acid sequence of the beta

```
RT   subunit.";
RL   J. Biol. Chem. 248:6810-6827(1973).
RN   [7]
RP   SEQUENCE OF 1-5 FROM N.A.
RX   MEDLINE=86195987; PubMed=2422163;
RA   Policastro P.F., Daniels-Mcqueen S., Carle G., Boime I.;
RT   "A map of the hCG beta-LH beta gene cluster.";
RL   J. Biol. Chem. 261:5907-5916(1986).
RN   [8]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE=81215630; PubMed=7240231;
RA   Mise T., Bahl O.P.;
RT   "Assignment of disulfide bonds in the beta subunit of human chorionic
RT   gonadotropin.";
RL   J. Biol. Chem. 256:6587-6592(1981).
RN   [9]
RP   DISULFIDE BONDS.
RX   MEDLINE=90094415; PubMed=1688430;
RA   Saccuzo Beebe J., Mountjoy K., Krzesicki R.F., Perini F.,
RA   Ruddon R.W.;
RT   "Role of disulfide bond formation in the folding of human chorionic
RT   gonadotropin beta subunit into an alpha beta dimer assembly-competent
RT   form.";
RL   J. Biol. Chem. 265:312-317(1990).
RN   [10]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE=92314469; PubMed=1820200;
RA   Weisshaar G., Hiyama J., Renwick A.G.C.;
RT   "Site-specific N-glycosylation of human chorionic gonadotrophin --
RT   structural analysis of glycopeptides by one- and two-dimensional 1H
RT   NMR spectroscopy.";
RL   Glycobiology 1:393-404(1991).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX   MEDLINE=94261179; PubMed=8202136;
RA   Lapthorn A.J., Harris D.C., Littlejohn A., Lustbader J.W.,
RA   Canfield R.E., Machin K.J., Morgan F.J., Isaacs N.W.;
RT   "Crystal structure of human chorionic gonadotropin.";
RL   Nature 369:455-461(1994).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
CC   -!- DEVELOPMENTAL STAGE: MADE BY THE FIRST TRIMESTER PLACENTA.
CC   -!- PHARMACEUTICAL: Available under the names Novarel (Ferring) and
CC       Profasi (Serono).
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00117; AAA96690.1; -.
DR   EMBL; X00265; CAA25068.1; ALT_INIT.
DR   EMBL; X00266; CAA25069.1; ALT_INIT.
DR   EMBL; M13504; AAA52005.1; -.
DR   EMBL; M13505; AAA52008.1; -.
DR   EMBL; M13503; AAA52009.1; -.
DR   EMBL; K03189; AAA53288.1; -.
DR   EMBL; K03187; AAA53288.1; JOINED.
DR   EMBL; K03188; AAA53288.1; JOINED.
DR   EMBL; K03183; AAA53287.1; -.
DR   EMBL; K00092; AAA53287.1; JOINED.
DR   EMBL; K03182; AAA53287.1; JOINED.
DR   PIR; A01502; KTHUB.
DR   PDB; 1HCN; 30-SEP-94.
DR   PDB; 1HRP; 01-NOV-94.
DR   PDB; 1XUL; 15-MAY-97.
DR   GlycoSuiteDB; P01233; -.
DR   Genew; HGNC:1886; CGB.
DR   Genew; HGNC:16451; CGB7.
DR   Genew; HGNC:16452; CGB5.
DR   MIM; 118860; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Glycoprotein; Signal; Pharmaceutical; 3D-structure.
FT   SIGNAL       1     20
FT   CHAIN       21    165       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID    29     77
FT   DISULFID    43     92
FT   DISULFID    46    130
FT   DISULFID    54    108
FT   DISULFID    58    110
FT   DISULFID   113    120
FT   CARBOHYD    33     33       N-LINKED (GLCNAC. . .).
FT                               /FTId=CAR_000042.
FT   CARBOHYD    50     50       N-LINKED (GLCNAC. . .).
FT                               /FTId=CAR_000043.
FT   CARBOHYD   141    141       O-LINKED.
FT   CARBOHYD   147    147       O-LINKED.
FT   CARBOHYD   152    152       O-LINKED.
FT   CARBOHYD   158    158       O-LINKED.
FT   VARIANT    137    137       D -> A (IN GENE 6).
FT                               /FTId=VAR_003188.
FT   CONFLICT    24     24       P -> M (IN REF. 3; AAA53287).
SQ   SEQUENCE   165 AA;  17739 MW;  5598FB9E51A05748 CRC64;

  Query Match             80.6%;  Score 793;  DB 1;  Length 165;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-60;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
           |||||||||||||||||||||||
Db     142 KAPPPSLPSPSRLPGPSDTPILPQ 165


RESULT 2
CGHB_PAPAN
ID   CGHB_PAPAN     STANDARD;      PRT;   165 AA.
AC   P07434;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-APR-1988 (Rel. 07, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Choriogonadotropin beta chain precursor (Chorionic gonadotrophin beta
DE   subunit) (CG-beta).
GN   CGB.
OS   Papio anubis (Olive baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Papio.
OX   NCBI_TaxID=9555;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87106851; PubMed=2433190;
RA   Crawford R.J., Tregear G.W., Niall H.D.;
```

```
RT   "The nucleotide sequences of baboon chorionic gonadotropin
RT   beta-subunit genes have diverged from the human.";
RL   Gene 46:161-169(1986).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
CC   -!- MISCELLANEOUS: THERE ARE AT LEAST FIVE COPIES OF CG-RELATED GENES
CC       AND AT LEAST TWO OF THESE ARE EXPRESSED IN THE BABOON PLACENTA.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M14966; AAA35383.1; -.
DR   PIR; A25808; KTBAB.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Glycoprotein; Signal.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   CHAIN        21    165       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD     50     50       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    141    141       O-LINKED (BY SIMILARITY).
FT   CARBOHYD    147    147       O-LINKED (BY SIMILARITY).
FT   CARBOHYD    152    152       O-LINKED (BY SIMILARITY).
SQ   SEQUENCE   165 AA;  17592 MW;  36D3E207A9F1E1C3 CRC64;

  Query Match             66.2%;  Score 651;  DB 1;  Length 165;
  Best Local Similarity   79.2%;  Pred. No. 5.4e-48;
  Matches  118;  Conservative   10;  Mismatches   21;  Indels    0;  Gaps    0;

Qy      21 GCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVV 80
           | :  :||||| |||||||||| ||| ||||:||||||||||||| |||| ||| :||||
Db      17 GAQASREPLRPLCRPINATLAAEKEACPVCVTVNTTICAGYCPTMMRVLQAVLPPVPQVV 76

Qy      81 CNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQ 140
           ||||:|||||||||||| ||:|:||  |||||:|||||||:|||||||||||||  |
Db      77 CNYREVRFESIRLPGCPPGVDPMVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPNLQ 136

Qy     141 DSSSSKAPPPSLPSPSRLPGPSDTPILPQ 169
           ||||| |||| |||||| |: || |||
Db     137 ASSSSKDPPPSPPSPSRLLEPAGTPFLPQ 165


RESULT 3
LSHB_HUMAN
ID   LSHB_HUMAN     STANDARD;      PRT;   141 AA.
AC   P01229;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE   beta) (LSH-B) (LH-B).
GN   LHB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84093590; PubMed=6690982;
RA   Talmadge K., Vamvakopoulos N.C., Fiddes J.C.;
RT   "Evolution of the genes for the beta subunits of human chorionic
RT   gonadotropin and luteinizing hormone.";
RL   Nature 307:37-40(1984).
RN   [2]
RP   SEQUENCE OF 21-141.
RX   MEDLINE=76062547; PubMed=1191677;
RA   Sairam M.R., Li C.H.;
RT   "Human pituitary lutropin. Isolation, properties, and the complete
RT   amino acid sequence of the beta-subunit.";
RL   Biochim. Biophys. Acta 412:70-81(1975).
RN   [3]
RP   PRELIMINARY SEQUENCE OF 21-141.
RX   MEDLINE=73090987; PubMed=4685398;
RA   Shome B., Parlow A.F.;
RT   "The primary structure of the hormone-specific, beta subunit of human
RT   pituitary luteinizing hormone (hLH).";
RL   J. Clin. Endocrinol. Metab. 36:618-621(1973).
RN   [4]
RP   PRELIMINARY PARTIAL SEQUENCE.
RX   MEDLINE=73221227; PubMed=4719207;
RA   Closset J., Hennen G., Lequin R.M.;
RT   "Human luteinizing hormone. The amino acid sequence of the
RT   subunit.";
RL   FEBS Lett. 29:97-100(1973).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATE.
RX   MEDLINE=91122088; PubMed=1991473;
RA   Weisshaar G., Hiyama J., Renwick A.G.C., Nimtz M.;
RT   "NMR investigations of the N-linked oligosaccharides at individual
RT   glycosylation sites of human lutropin.";
RL   Eur. J. Biochem. 195:257-268(1991).
RN   [6]
RP   STRUCTURE BY NMR OF 58-77.
RX   MEDLINE=92357029; PubMed=1495492;
RA   Keutmann H.T., Hua Q.-X., Weiss M.A.;
RT   "Structure of a receptor-binding fragment from human luteinizing
RT   hormone beta-subunit determined by [1H]- and [15N]nuclear magnetic
RT   resonance spectroscopy.";
RL   Mol. Endocrinol. 6:904-913(1992).
RN   [7]
RP   VARIANT ARG-74.
RX   MEDLINE=92085985; PubMed=1727547;
RA   Weiss J., Axelrod L., Whitcomb R.W., Harris P.E., Crowley W.F.,
RA   Jameson J.L.;
RT   "Hypogonadism caused by a single amino acid substitution in the beta
RT   subunit of luteinizing hormone.";
RL   New Engl. J. Med. 326:179-183(1992).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PITUITARY.
CC   -!- DISEASE: DEFECTS IN LHB ARE A CAUSE OF HYPOGONADISM WHICH IS
CC       CHARACTERIZED BY INFERTILITY AND PSEUDOHERMAPHRODITISM.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
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CC   ----------------------------------------------------------------------------
DR   EMBL; X00264; CAA25067.1; -.
DR   EMBL; S71273; AAD14960.1; ALT_SEQ.
DR   PIR; A01497; UTHUB.
DR   HSSP; P01233; 1XUL.
DR   GlycoSuiteDB; P01229; -.
DR   Genew; HGNC:6584; LHB.
DR   MIM; 152780; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Glycoprotein; Signal; Pseudohermaphroditism;
KW   Disease mutation.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     50     50       N-LINKED (GLCNAC. . .).
FT                                /FTId=CAR_000045.
FT   VARIANT      74     74       Q -> R (IN HYPOGONADISM; LACK OF
FT                                RECEPTOR-BINDING).
FT                                /FTId=VAR_003189.
FT   CONFLICT     39     39       E -> Q (IN REF. 2).
FT   CONFLICT     76     76       MISSING (IN REF. 2).
FT   CONFLICT    132    135       HPQL -> PQH (IN REF. 2).
SQ   SEQUENCE   141 AA;  15345 MW;  E411766253113F7C CRC64;

  Query Match             54.9%;  Score 540;  DB 1;  Length 141;
  Best Local Similarity   85.0%;  Pred. No. 9e-39;
  Matches   96;  Conservative    6;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           :|||||  | |||| ||||||||||||||||||||||||| |||| ||| |||||| |||
Db      22 REPLRPWCHPINAILAVEKEGCPVCITVNTTICAGYCPTMMRVLQAVLPPLPQVVCTYRD 81

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPR 138
           ||||||||||||||:||||: |||||:|  |||||:||||||||||||| |:
Db      82 VRFESIRLPGCPRGVDPVVSFPVALSCRCGPCRRRSTSDCGGPKDHPLTCDHPQ 134


RESULT 4
CGHB_CALJA
ID   CGHB_CALJA     STANDARD;      PRT;   164 AA.
AC   P51500;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Choriogonadotropin beta chain precursor (Chorionic gonadotrophin beta
DE   subunit) (CG-beta).
GN   CGB.
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC   Callithrix.
OX   NCBI_TaxID=9483;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=96115012; PubMed=7492691;
RA   Simula A.P., Amato F., Faast R., Lopata A., Berka J., Norman R.J.;
RT   "Luteinizing hormone/chorionic gonadotropin bioactivity in the common
RT   marmoset (Callithrix jacchus) is due to a chorionic gonadotropin
RT   molecule with a structure intermediate between human chorionic
RT   gonadotropin and human luteinizing hormone.";
RL   Biol. Reprod. 53:380-389(1995).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ----------------------------------------------------------------------------
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CC   ----------------------------------------------------------------------------
DR   EMBL; U04447; AAC00029.1; -.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Glycoprotein; Signal.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   CHAIN        21    164       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     50     50       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    146    146       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    151    151       O-LINKED (BY SIMILARITY).
SQ   SEQUENCE   164 AA;  17712 MW;  0CD92EDDC2618FA6 CRC64;

  Query Match             52.5%;  Score 516.5;  DB 1;  Length 164;
  Best Local Similarity   66.0%;  Pred. No. 9.7e-37;
  Matches   95;  Conservative   17;  Mismatches   31;  Indels    1;  Gaps    1;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           |||||| |||:|| || ||||||||:  ||||||||| :| |||| :|| ||| |||| :
Db      22 KEPLRPLCRPVNAILAAEKEGCPVCVAFNTTICAGYCSSMVRVLQTILPPLPQSVCNYHE 81

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           :|| |:|||||  ||:|||| |||||:| ||||| :||| :: || ||   ||| |||
Db      82 LRFTSVRLPGCRPGVDPVVSMPVALSCRCGLCRRSYSDCGSLRNEPLGCDYSTFQD-SSS 140

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
           | || :| |||:|  |:| |::||
Db     141 KDPPRNLTSPSQLLEPADPPLVPQ 164


RESULT 5
LSHB_EQUBU
ID   LSHB_EQUBU     STANDARD;      PRT;   169 AA.
AC   O46641;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Lutropin/choriogonadotropin beta chain precursor (LSH-B/CG-B)
DE   (Lutenizing hormone beta subunit).
GN   LHB.
OS   Equus burchelli (Plains zebra) (Equus quagga).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9790;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pituitary;
RX   MEDLINE=99273280; PubMed=10341734;
RA   Chopineau M., Martinat N., Pourchet C., Stewart F., Combarnous Y.,
RA   Guillou F.;
RT   "Cloning, sequencing and functional expression of zebra (Equus
RT   burchelli) LH.";
RL   J. Reprod. Fertil. 115:159-166(1999).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y16265; CAA76146.1; -.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Glycoprotein; Signal.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   CHAIN        21    169       LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    158    158       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   169 AA;  17824 MW;  322DF724AEAA93E9 CRC64;

  Query Match             48.4%;  Score 476;  DB 1;  Length 169;
  Best Local Similarity   57.6%;  Pred. No. 2.5e-33;
  Matches   91;  Conservative   17;  Mismatches   34;  Indels   16;  Gaps    4;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| ||||||||| ||| ||:||| |:|||||||:| ||:   || :
Db      19 WASRG------PLRPLCRPINATLAAEKEACPICITFTTSICAGYCPSMVRVMPAALPPI 72

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
           || || ||::|| |||||||| ||:|:||: ||||| |  ||  |||||||:|||| |
Db      73 PQPVCTYRELRFASIRLPGCPPGVDPMVSFPVALSCHCGPCRLKTTDCGGPRDHPLACAP 132

Qy     137 PRFQDSSSSKAPP--PSLPSPSRLPGPSDTPILPQTSH 172
             | ||||| ||  |   : :  || |:     ::||
Db     133 ---QASSSSKDPPSQPLTSTSTPTPGASN-----RSSH 162


RESULT 6
LSHB_EQUAS
ID   LSHB_EQUAS     STANDARD;      PRT;   169 AA.
AC   P19794;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Lutropin/choriogonadotropin beta chain precursor (LSH-B/CG-B)
DE   (Lutenizing hormone beta subunit).
GN   LHB.
OS   Equus asinus (Donkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9793;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chopineau M., Combarnous Y., Allen W.R., Stewart F.;
RL   Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   PRELIMINARY SEQUENCE OF 105-169 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=90262634; PubMed=2344391;
RA   Leigh S.E.A., Stewart F.;
RT   "Partial cDNA sequence for the donkey chorionic gonadotrophin-beta
RT   subunit suggests evolution from an ancestral LH-beta gene.";
RL   J. Mol. Endocrinol. 4:143-150(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X80116; CAA56422.1; -.
DR   EMBL; X53669; CAA37709.1; ALT_SEQ.
DR   PIR; S15676; S15676.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Glycoprotein; Signal.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   CHAIN        21    169       LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .) (PROBABLE).
SQ   SEQUENCE   169 AA;  17943 MW;  AEED20891E96FA7C CRC64;

  Query Match             46.8%;  Score 461;  DB 1;  Length 169;
  Best Local Similarity   55.1%;  Pred. No. 4.4e-32;
  Matches   86;  Conservative   16;  Mismatches   40;  Indels   14;  Gaps    2;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| ||||||||| ||| ||:||| |:|||||| :| ||:   || :
Db      19 WASRG------PLRPLCRPINATLAAEKEACPICITFTTSICAGYCRSMVRVMPAALPPI 72

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPL---- 132
           || || ||::|| |||||||| ||:|:||: ||||| |  ||  |||||||:||||
Db      73 PQPVCTYRELRFGSIRLPGCPPGVDPMVSFPVALSCHCGPCRLKTTDCGGPRDHPLACAP 132
```

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Qy    133 ----TCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDT 164
              :| ||  |  :|:  | |     |  | | :|
Db    133 QTSSSCKDPPSQPLTSTSTPTPGASRRSSHPLPINT 168


RESULT 7
LSHB_HORSE
ID   LSHB_HORSE     STANDARD;      PRT;   169 AA.
AC   P08751; P01234;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lutropin/choriogonadotropin beta chain precursor (LSH-B/CG-B)
DE   (Lutenizing hormone beta subunit).
GN   LHB.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92357035; PubMed=1379674;
RA   Sherman G.B., Wolfe M.W., Farmerie T.A., Clay C.M.,
RA   Threadgill D.S., Sharp D.C., Nilson J.H.;
RT   "A single gene encodes the beta-subunits of equine luteinizing
RT   hormone and chorionic gonadotropin.";
RL   Mol. Endocrinol. 6:951-959(1992).
RN   [2]
RP   SEQUENCE OF 21-169.
RX   MEDLINE=87250476; PubMed=3298239;
RA   Bousfield G.R., Liu W.-K., Sugino H., Ward D.N.;
RT   "Structural studies on equine glycoprotein hormones. Amino acid
RT   sequence of equine lutropin beta-subunit.";
RL   J. Biol. Chem. 262:8610-8620(1987).
RN   [3]
RP   SEQUENCE OF 21-169.
RX   MEDLINE=87250475; PubMed=3298238;
RA   Sugino H., Bousfield G.R., Moore W.T. Jr., Ward D.N.;
RT   "Structural studies on equine glycoprotein hormones. Amino acid
RT   sequence of equine chorionic gonadotropin beta-subunit.";
RL   J. Biol. Chem. 262:8603-8609(1987).
RN   [4]
RP   PARTIAL SEQUENCE.
RA   Ward D.N., Moore W.T. Jr., Burleigh B.D.;
RT   "Structural studies on equine chorionic gonadotropin.";
RL   J. Protein Chem. 1:263-280(1982).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE=90235854; PubMed=2331995;
RA   Damm J.B.L., Haard K., Kamerling J.P., van Dedem G.W.K.,
RA   Vliegenthart J.F.G.;
RT   "Structure determination of the major N- and O-linked carbohydrate
RT   chains of the beta subunit from equine chorionic gonadotropin.";
RL   Eur. J. Biochem. 189:175-183(1990).
RN   [6]
RP   O-GLYCOSYLATION.
RX   PubMed=11133668;
RA   Bousfield G.R., Butnev V.Y., Butnev V.Y.;
RT   "Identification of twelve O-glycosylation sites in equine chorionic
RT   gonadotropin beta and equine luteinizing hormone beta by solid-phase
RT   Edman degradation.";
RL   Biol. Reprod. 64:136-147(2001).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- PTM: MICROHETEROGENEITY AT ASN-33. O-GLYCOSYLATION APPEARS TO BE
CC       RESPONSIBLE FOR THE BETA SUBUNIT CONTRIBUTION TO THE DIFFERENCE IN
CC       LH RECEPTOR-BINDING ACTIVITY BETWEEN LSH-B AND CG-B.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S41704; AAB22775.1; -.
DR   PIR; A01503; KTHOB.
DR   PIR; A29304; A29304.
DR   PIR; A29305; A29305.
DR   PIR; A41917; A41917.
DR   HSSP; P01233; 1XUL.
DR   GlycoSuiteDB; P08751; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Glycoprotein; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    169       LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    138    138       O-LINKED (GALNAC. . .).
FT   CARBOHYD    143    143       O-LINKED (GALNAC. . .).
FT   CARBOHYD    147    147       O-LINKED (GALNAC. . .).
FT   CARBOHYD    148    148       O-LINKED (GALNAC. . .).
FT   CARBOHYD    149    149       O-LINKED (GALNAC. . .).
FT   CARBOHYD    150    150       O-LINKED (GALNAC. . .).
FT   CARBOHYD    151    151       O-LINKED (GALNAC. . .).
FT   CARBOHYD    153    153       O-LINKED (GALNAC. . .).
FT   CARBOHYD    157    157       O-LINKED (GALNAC. . .).
FT   CARBOHYD    160    160       O-LINKED (GALNAC. . .).
FT   CARBOHYD    161    161       O-LINKED (GALNAC. . .).
FT   CARBOHYD    169    169       O-LINKED (GALNAC. . .).
SQ   SEQUENCE   169 AA;  17865 MW;  1244ADBEB843EF1A CRC64;

  Query Match             45.3%;  Score 446;  DB 1;  Length 169;
  Best Local Similarity   55.0%;  Pred. No. 8e-31;
  Matches   88;  Conservative   17;  Mismatches   41;  Indels   14;  Gaps    3;

Qy     17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
          | : |      |||| |||||||||| ||| ||:||| |:||||||||:| ||:   |||:
Db     19 WASRG------PLRPLCRPINATLAAEKEACPICITFTTSICAGYCPSMVRVMPAALPAI 72

Qy     77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
          || || ||::|| |||||||| ||:|:||: ||||| |  |:  |||||  :| || |
Db     73 PQPVCTYRELRFASIRLPGCPPGVDPMVSFPVALSCHCGPCQIKTTDCGVFRDQPLACAP 132

Qy    137 PRFQDSSSSKAPPPSLPSPSRLPGP-----SDTPILPQTS 171
             | ||||| ||    : :  | |      |  |:  :||
Db    133 ---QASSSSKDPPSQPLTSTSTPTPGASRRSSHPLPIKTS 169


RESULT 8
LSHB_FELCA
ID   LSHB_FELCA     STANDARD;      PRT;   143 AA.
AC   O77805;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE   beta) (LSH-B) (LH-B).
```

```
GN   LHB.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pituitary;
RA   Pukazhenthi B.S., Varma G.M., Brown J.L.;
RT   "Molecular cloning and sequence analysis of the cDNA for the feline
RT   luteinizing hormone beta subunit.";
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF095716; AAC64196.1; -.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    143       LUTROPIN BETA CHAIN.
FT   DISULFID     31     79       BY SIMILARITY.
FT   DISULFID     45     94       BY SIMILARITY.
FT   DISULFID     48    132       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
FT   DISULFID    115    122       BY SIMILARITY.
FT   CARBOHYD     35     35       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   143 AA;  15318 MW;  C5C55DDC907422DB CRC64;

  Query Match             45.1%;  Score 444;  DB 1;  Length 143;
  Best Local Similarity   67.9%;  Pred. No. 9.9e-31;
  Matches   76;  Conservative   13;  Mismatches   23;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           :||||| |||||||||  | | ||||:|  |||||||||:| |||   || :|| || ||:
Db      24 REPLRPLCRPINATLAAENEACPVCVTFTTTICAGYCPSMMRVLPAALPPVPQPVCTYRE 83

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 137
           :|| |:|||||| ||:|||||: |||||:|  || |::||||||:  || || |
Db      84 LRFASVRLPGCPPGVDPVVSFPVALSCRCGPCRLSSSDCGGPRAQPLACDRP 135


RESULT 9
LSHB_BOVIN
ID   LSHB_BOVIN     STANDARD;      PRT;   141 AA.
AC   P04651;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE   beta) (LSH-B) (LH-B).
GN   LHB.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85207729; PubMed=2987241;
RA   Virgin J.B., Silver B.J., Thomason A.R., Nilson J.H.;
RT   "The gene for the beta subunit of bovine luteinizing hormone encodes
RT   a gonadotropin mRNA with an unusually short 5'-untranslated region.";
RL   J. Biol. Chem. 260:7072-7077(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85182575; PubMed=3838746;
RA   Maurer R.A.;
RT   "Analysis of several bovine lutropin beta subunit cDNAs reveals
RT   heterogeneity in nucleotide sequence.";
RL   J. Biol. Chem. 260:4684-4687(1985).
RN   [3]
RP   SEQUENCE OF 21-139.
RX   MEDLINE=74075724; PubMed=4770795;
RA   Maghuin-Rogister G., Hennen G.;
RT   "Luteinizing hormone. The primary structures of the beta-subunit from
RT   bovine and porcine species.";
RL   Eur. J. Biochem. 39:235-253(1973).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M10077; AAA30623.1; -.
DR   EMBL; M11506; AAB59267.1; -.
DR   PIR; A01499; UTBOB.
DR   HSSP; P01233; 1XUL.
DR   GlycoSuiteDB; P04651; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .).
FT                                /FTId=CAR_000044.
FT   CONFLICT      1      2       MISSING (IN REF. 2).
FT   CONFLICT     74     74       Q -> E (IN REF. 3).
FT   CONFLICT    112    112       P -> S (IN REF. 2).
FT   CONFLICT    122    123       GP -> PG (IN REF. 3).
FT   CONFLICT    126    126       Q -> E (IN REF. 3).
SQ   SEQUENCE   141 AA;  15202 MW;  44FB1CBD4901BC95 CRC64;
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  Query Match           44.4%;  Score 437;  DB 1;  Length 141;
  Best Local Similarity  61.6%;  Pred. No. 3.8e-30;
  Matches   77;  Conservative   14;  Mismatches   28;  Indels    6;  Gaps    1;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| |:||||||| ||| ||||||  |:||||||:| |||  :|| :
Db      19 WASRG------PLRPLCQPINATLAAEKEACPVCITFTTSICAGYCPSMKRVLPVILPPM 72

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
           || || | ::|| |:|||||| ||:|:||: ||||| |  || |:||||||:  || ||
Db      73 PQRVCTYHELRFASVRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDH 132

Qy     137 PRFQD 141
           |   |
Db     133 PPLPD 137


RESULT 10
LSHB_RAT
ID   LSHB_RAT       STANDARD;      PRT;   141 AA.
AC   P01230;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE   beta) (LSH-B) (LH-B).
GN   LHB.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=83273673; PubMed=6192440;
RA   Chin W.W., Godine J.E., Klein D.R., Chang A.S., Tan L.K.,
RA   Habener J.F.;
RT   "Nucleotide sequence of the cDNA encoding the precursor of the beta
RT   subunit of rat lutropin.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4649-4653(1983).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85080043; PubMed=6096374;
RA   Jameson L., Chin W.W., Hollenberg A.N., Chang A.S., Habener J.F.;
RT   "The gene encoding the beta-subunit of rat luteinizing hormone.
RT   Analysis of gene structure and evolution of nucleotide sequence.";
RL   J. Biol. Chem. 259:15474-15480(1984).
RN   [3]
RP   SEQUENCE OF 4-141 FROM N.A.
RC   STRAIN=Wistar Imamichi; TISSUE=Anterior pituitary;
RA   Kato Y., Ezashi T., Hirai T., Kato T.;
RT   "Strain difference in nucleotide sequences of rat glycoprotein hormone
RT   subunit cDNAs and gene fragment.";
RL   Zool. Sci. 7:877-885(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V01542; CAA24783.1; -.
DR   EMBL; J00749; AAA96703.1; -.
DR   EMBL; D00576; BAA00454.1; -.
DR   PIR; A01498; UTRTB.
DR   PIR; S42527; S42527.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .) (PROBABLE).
SQ   SEQUENCE   141 AA;  15177 MW;  50796FB8E32F83BF CRC64;

  Query Match           44.1%;  Score 434;  DB 1;  Length 141;
  Best Local Similarity  62.0%;  Pred. No. 6.7e-30;
  Matches   75;  Conservative   16;  Mismatches   24;  Indels    6;  Gaps    1;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| ||||:||||| | | |||||  |:||||||:| |||   || :
Db      19 WASRG------PLRPLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPV 72

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
           || || ||::|| |:|||||| ||:|:||: |||||:|  || |::|||||:  |:|||
Db      73 PQPVCTYRELRFASVRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMTCDL 132

Qy     137 P 137
           |
Db     133 P 133


RESULT 11
LSHB_CERSI
ID   LSHB_CERSI     STANDARD;      PRT;   141 AA.
AC   O77835; O19102;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE   beta) (LSH-B) (LH-B).
GN   LHB1 AND LHB2.
OS   Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
OX   NCBI_TaxID=9807;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98389253; PubMed=9723860;
RA   Lund L.A., Sherman G.B.;
RT   "Duplication of the southern white rhinoceros (Ceratotherium simum
RT   simum) luteinizing hormone beta subunit gene.";
RL   J. Mol. Endocrinol. 21:19-30(1998).
RN   [2]
RP   SEQUENCE OF 7-141 FROM N.A.
RC   TISSUE=Pituitary;
RX   MEDLINE=97449288; PubMed=9305757;
RA   Sherman G.B., Lund L.A., Bunick D., Winn R.J.;
RT   "Characterization and phylogenetic significance of rhinoceros
RT   luteinizing hormone beta (LHbeta) subunit messenger RNA structure,
RT   complementary DNA sequence and gene copy number.";
RL   Gene 195:131-139(1997).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
```

```
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF024521; AAC36049.1; -.
DR   EMBL; AF024520; AAC36048.1; -.
DR   EMBL; U72659; AAB71983.1; -.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     22     22       R -> K (IN REF. 2).
SQ   SEQUENCE   141 AA;  14930 MW;  FFEDB157C51976C9 CRC64;

  Query Match             43.5%;  Score 428;  DB 1;  Length 141;
  Best Local Similarity   62.8%;  Pred. No. 2.1e-29;
  Matches   76;  Conservative   12;  Mismatches   27;  Indels    6;  Gaps    1;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| ||||||||| | | ||||||  |:|||||||:| |||   ||
Db      19 WASRG------PLRPLCRPINATLAAENEACPVCITFTTSICAGYCPSMVRVLPAALPPA 72

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
           || || | ::|| |||||||| ||:|:||: |||||:|  || |::|||||:  || ||
Db      73 PQPVCTYHELRFASIRLPGCPPGVDPMVSFPVALSCRCGPCRLSSSDCGGPRAQPLACDR 132

Qy     137 P 137
           |
Db     133 P 133


RESULT 12
LSHB_PIG
ID   LSHB_PIG       STANDARD;      PRT;   141 AA.
AC   P01232;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE   beta) (LSH-B) (LH-B).
GN   LHB.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91063934; PubMed=1701088;
RA   Ezashi T., Hirai T., Kato T., Wakabayashi K., Kato Y.;
RT   "The gene for the beta subunit of porcine LH: clusters of GC boxes
RT   and CACCC elements.";
RL   J. Mol. Endocrinol. 5:137-146(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89306142; PubMed=2744222;
RA   Kato Y., Hirai T.;
RT   "Cloning and DNA sequence analysis of the cDNA for the precursor of
RT   porcine luteinizing hormone (LH) beta subunit.";
RL   Mol. Cell. Endocrinol. 62:47-53(1989).
RN   [3]
RP   SEQUENCE OF 21-139.
RX   MEDLINE=74075724; PubMed=4770795;
RA   Maghuin-Rogister G., Hennen G.;
RT   "Luteinizing hormone. The primary structures of the beta-subunit from
RT   bovine and porcine species.";
RL   Eur. J. Biochem. 39:235-253(1973).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D00579; BAA00457.1; -.
DR   PIR; A30322; UTPGB.
DR   PIR; A48170; A48170.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .).
FT   MOD_RES      21     21       BLOCKED.
FT   VARIANT      30     30       R -> Z.
FT   CONFLICT     40     40       N -> D (IN REF. 3).
FT   CONFLICT     62     62       V -> R (IN REF. 3).
FT   CONFLICT     83     83       S -> I (IN REF. 3).
FT   CONFLICT     87     87       I -> S (IN REF. 3).
FT   CONFLICT    122    123       GP -> PG (IN REF. 3).
SQ   SEQUENCE   141 AA;  14889 MW;  803E8E7C59F3C2CF CRC64;

  Query Match             43.4%;  Score 427;  DB 1;  Length 141;
  Best Local Similarity   62.8%;  Pred. No. 2.6e-29;
  Matches   76;  Conservative   11;  Mismatches   28;  Indels    6;  Gaps    1;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| ||||||||| | | ||||||  |:|||||||:| |||   || :
Db      19 WASRG------PLRPLCRPINATLAAENEACPVCITFTTSICAGYCPSMVRVLPAALPPV 72

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
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Db     73 PQPVCTYRELSFASIRLPGCPPGVDPTVSFPVALSCHCGPCRLSSSDCGGPRAQPLACDR 132

Qy    137 P 137
          |
Db    133 P 133


RESULT 13
LSHB_SHEEP
ID   LSHB_SHEEP     STANDARD;      PRT;   141 AA.
AC   P01231;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE   beta) (LSH-B) (LH-B) (Interstitial cell stimulating hormone).
GN   LHB.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93351742; PubMed=8349025;
RA   Brown P., McNeilly J.R., Wallace R.M., McNeilly A.S., Clark A.J.;
RT   "Characterization of the ovine LH beta-subunit gene: the promoter
RT   directs gonadotrope-specific expression in transgenic mice.";
RL   Mol. Cell. Endocrinol. 93:157-165(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pituitary;
RX   MEDLINE=90245669; PubMed=2336396;
RA   D'Angelo-Bernard G., Moumni M., Jutisz M., Counis R.;
RT   "Cloning and sequence analysis of the cDNA for the precursor of the
RT   beta subunit of ovine luteinizing hormone.";
RL   Nucleic Acids Res. 18:2175-2175(1990).
RN   [3]
RP   SEQUENCE OF 21-139.
RX   MEDLINE=72211145; PubMed=4556309;
RA   Liu W.-K., Nahm H.S., Sweeney C.M., Holcomb G.N., Ward D.N.;
RT   "The primary structure of ovine luteinizing hormone. II. The amino
RT   acid sequence of the reduced, S-carboxymethylated A-subunit (LH-
RT   beta).";
RL   J. Biol. Chem. 247:4365-4381(1972).
RN   [4]
RP   SEQUENCE OF 21-139.
RX   MEDLINE=73190035; PubMed=4575435;
RA   Sairam M.R., Samy T.S.A., Papkoff H., Li C.H.;
RT   "The primary structure of ovine interstitial cell-stimulating
RT   hormone. II. The beta-subunit.";
RL   Arch. Biochem. Biophys. 153:572-586(1972).
RN   [5]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE=76068152; PubMed=1201911;
RA   Chung D., Sairam M.R., Li C.H.;
RT   "The primary structure of ovine interstitial cell stimulating
RT   hormone. IV: Disulfide bridges of the beta subunit.";
RL   Int. J. Pept. Protein Res. 7:487-493(1975).
RN   [6]
RP   STRUCTURE OF CARBOHYDRATE.
RX   MEDLINE=91006170; PubMed=2209620;
RA   Weisshaar G., Hiyama J., Renwick A.G.C.;
RT   "Site-specific N-glycosylation of ovine lutropin. Structural analysis
RT   by one- and two-dimensional 1H-NMR spectroscopy.";
RL   Eur. J. Biochem. 192:741-751(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC     , CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S64695; AAB27819.1; -.
DR   EMBL; X52488; CAA36729.1; -.
DR   PIR; A01500; UTSHB.
DR   PIR; S09232; S09232.
DR   HSSP; P01233; 1XUL.
DR   GlycoSuiteDB; P01231; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92
FT   DISULFID     46    130
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120
FT   MOD_RES      21     21       BLOCKED.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .).
FT                                /FTId=CAR_000046.
FT   VARIANT     138    141       MISSING (IN SOME MOLECULES).
FT   CONFLICT     30     30       Q -> E (IN REF. 4).
FT   CONFLICT     59     59       L -> P (IN REF. 1).
FT   CONFLICT     63     63       R -> Q (IN REF. 2).
FT   CONFLICT     71     71       P -> PP (IN REF. 4).
FT   CONFLICT     81     81       E -> Q (IN REF. 4).
FT   CONFLICT    122    123       GP -> PG (IN REF. 3 AND 4).
FT   CONFLICT    126    126       Q -> E (IN REF. 3 AND 4).
SQ   SEQUENCE   141 AA;  15184 MW;  C59EC7C0AA55A9DC CRC64;

  Query Match             43.4%;  Score 427;  DB 1;  Length 141;
  Best Local Similarity   60.8%;  Pred. No. 2.6e-29;
  Matches   76;  Conservative   14;  Mismatches   29;  Indels    6;  Gaps    1;

Qy     17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
          | : |      |||| |:||||||| ||| ||||||  |:|||||| :| |||  :|| :
Db     19 WASRG------PLRPLCQPINATLAAEKEACPVCITFTTSICAGYCLSMKRVLPVILPPM 72

Qy     77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
          || || | ::|| |:|||||| ||:|:||: ||||| |  || |:|||||:  || ||
Db     73 PQRVCTYHELRFASVRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDH 132

Qy    137 PRFQD 141
          |   |
Db    133 PPLPD 137


RESULT 14
LSHB_MOUSE
ID   LSHB_MOUSE     STANDARD;      PRT;   141 AA.
AC   O09108; Q60844;
DT   01-NOV-1997 (Rel. 35, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE   beta) (LSH-B) (LH-B).
GN   LHB.
```

```
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv;
RX   MEDLINE=96125216; PubMed=8543188;
RA   Kumar T.R., Matzuk M.M.;
RT   "Cloning of the mouse gonadotropin beta-subunit-encoding genes, II.
RT   Structure of the luteinizing hormone beta-subunit-encoding genes.";
RL   Gene 166:335-336(1995).
RN   [2]
RP   SEQUENCE OF 18-122 FROM N.A.
RC   STRAIN=C57BL/6 X CBA; TISSUE=Anterior pituitary;
RA   Brown P., Brooks J., McNeilly J.R., McNeilly A.S.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U25145; AAA92841.1; -.
DR   EMBL; Y10418; CAA71445.1; -.
DR   HSSP; P01233; 1XUL.
DR   MGD; MGI:96782; Lhb.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     83     83       A -> R (IN REF. 2).
SQ   SEQUENCE   141 AA;  15028 MW;  5E997CABF33D90BF CRC64;

  Query Match             43.0%;  Score 423;  DB 1;  Length 141;
  Best Local Similarity   60.3%;  Pred. No. 5.6e-29;
  Matches   73;  Conservative   16;  Mismatches   26;  Indels    6;  Gaps    1;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| |||:||||| | | ||||||  |:|||||||:| |||   || :
Db      19 WASRG------PLRPLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPV 72

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
           || || ||:: | |:|||||| ||:|:||: |||||:|  || |::|||||:  |: ||
Db      73 PQPVCTYRELAFASVRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMACDL 132

Qy     137 P 137
           |
Db     133 P 133


RESULT 15
LSHB_CANFA
ID   LSHB_CANFA     STANDARD;      PRT;   138 AA.
AC   P18842;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE   beta) (LSH-B) (LH-B) (Fragment).
GN   LHB.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88096605; PubMed=3697104;
RA   Wolf D.L., Appleby V.L., Hjerrild K., Baker A.R., Talmadge K.;
RT   "Nucleic acid and amino acid sequences of dog beta LH: comparison to
RT   rat, cow and human beta LH.";
RL   Nucleic Acids Res. 15:10602-10602(1987).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y00518; CAA68572.1; -.
DR   PIR; S00512; S00512.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Signal; Glycoprotein.
FT   NON_TER       1      1
FT   SIGNAL       <1     17
FT   CHAIN        18    138       LUTROPIN BETA CHAIN.
FT   DISULFID     26     74       BY SIMILARITY.
FT   DISULFID     40     89       BY SIMILARITY.
FT   DISULFID     43    127       BY SIMILARITY.
FT   DISULFID     51    105       BY SIMILARITY.
FT   DISULFID     55    107       BY SIMILARITY.
FT   DISULFID    110    117       BY SIMILARITY.
FT   CARBOHYD     30     30       N-LINKED (GLCNAC. . .) (PROBABLE).
SQ   SEQUENCE   138 AA;  14594 MW;  E3639FE6B03F1948 CRC64;

  Query Match             42.7%;  Score 420;  DB 1;  Length 138;
  Best Local Similarity   62.0%;  Pred. No. 9.7e-29;
  Matches   75;  Conservative   11;  Mismatches   29;  Indels    6;  Gaps    1;

Qy    . 17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| |||||||| | | ||||||  |||||||||:| |||   || :
Db      16 WASRG------PLRPLCRPINATLAAENEACPVCITFTTTICAGYCPSMVRVLPAALPPV 69

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
           || || | :: | |||||||| ||:|:||: |||||:|  || | :|||||:   | ||
Db      70 PQPVCTYHELHFASIRLPGCPPGVDPMVSFPVALSCRCGPCRLSNSDCGGPRAQSLACDR 129

Qy     137 P 137
           |
Db     130 P 130
```

Search completed: November 20, 2002, 17:27:58
Job time : 7.01399 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:27 ; Search time 21.8671 Seconds
(without alignments)
1667.815 Million cell updates/sec

Title: US-09-787-494-2
Perfect score: 984
Sequence: 1 MTMITDSLAVVLQRRDWENP.....LPGPSDTPILPQTSHHHHHH 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	788	80.1	159	4	Q8WTT5	Q8wtt5 homo sapien
2	783	79.6	159	4	Q8WXL2	Q8wxl2 homo sapien
3	776	78.9	159	4	Q8WXL3	Q8wxl3 homo sapien
4	764	77.6	159	4	Q8WXL4	Q8wxl4 homo sapien
5	758	77.0	159	4	Q8WXL1	Q8wxl1 homo sapien
6	738	75.0	157	6	Q8WNC5	Q8wnc5 pongo pygma
7	737	74.9	157	6	Q8WNC4	Q8wnc4 pongo pygma
8	735	74.7	157	6	Q8WNC7	Q8wnc7 pongo pygma
9	726	73.8	157	6	Q8WNC6	Q8wnc6 pongo pygma
10	657	66.8	165	6	Q9BEH1	Q9beh1 macaca fasc
11	654	66.5	159	6	Q8WNB0	Q8wnb0 macaca mula
12	653	66.4	159	6	Q8WNA9	Q8wna9 macaca mula
13	652	66.3	165	6	Q9BEH2	Q9beh2 macaca fasc
14	646	65.7	159	6	Q8WNB2	Q8wnb2 colobus gue
15	646	65.7	159	6	Q8WNA8	Q8wna8 macaca mula
16	644	65.4	159	6	Q8WNB1	Q8wnb1 colobus gue
17	642	65.2	165	6	Q9GL37	Q9gl37 macaca mula
18	642	65.2	165	11	Q99P48	Q99p48 mus musculu
19	631	64.1	159	6	Q8WNB3	Q8wnb3 colobus gue
20	628	63.8	159	6	Q8WNB4	Q8wnb4 colobus gue
21	616	62.6	157	6	Q8WNB9	Q8wnb9 presbytis o
22	615	62.5	157	6	Q8WNC3	Q8wnc3 presbytis o
23	609	61.9	157	6	Q8WNC0	Q8wnc0 presbytis o
24	608.5	61.8	157	6	Q8WNC1	Q8wnc1 presbytis o
25	605	61.5	157	6	Q8WNC2	Q8wnc2 presbytis o
26	574	58.3	136	6	Q8WNB8	Q8wnb8 pongo pygma
27	540	54.9	136	4	Q8WXL0	Q8wxl0 homo sapien
28	515	52.3	136	6	Q8WNB6	Q8wnb6 presbytis o
29	505	51.3	136	6	Q8WNB5	Q8wnb5 colobus gue
30	498.5	50.7	156	6	Q8WNA6	Q8wna6 aotus trivi
31	498	50.6	136	6	Q8WNB7	Q8wnb7 macaca mula
32	476.5	48.4	156	6	Q8WNA7	Q8wna7 callicebus
33	446	45.3	142	6	Q9BDI9	Q9bdi9 panthera ti
34	441	44.8	136	6	Q8WNA5	Q8wna5 tarsius ban
35	439	44.6	136	6	Q8WNA2	Q8wna2 galago sene
36	437	44.4	136	6	Q8WNA4	Q8wna4 daubentonia
37	434	44.1	136	6	Q8WNA3	Q8wna3 lemur varie
38	433	44.0	139	11	Q62778	Q62778 rattus norv
39	433	44.0	141	6	Q8WN18	Q8wn18 ailuropoda
40	431	43.8	136	6	Q8WNA0	Q8wna0 cynocephalu
41	430	43.7	136	6	Q8WNA1	Q8wna1 loris tardi
42	413	42.0	136	6	Q8WN99	Q8wn99 pteropus ly
43	398	40.4	127	11	Q924A6	Q924a6 cavia porce
44	398	40.4	135	11	Q924A7	Q924a7 cavia porce
45	398	40.4	141	11	Q924A8	Q924a8 cavia porce

ALIGNMENTS

RESULT 1
Q8WTT5
ID Q8WTT5 PRELIMINARY; PRT; 159 AA.
AC Q8WTT5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
RT evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF397577; AAL69705.1; -.
DR EMBL; AF397580; AAL69708.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 1
FT NON_TER 159 159
SQ SEQUENCE 159 AA; 16944 MW; 246BA938796A1727 CRC64;

Query Match 80.1%; Score 788; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.7e-74;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     17 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 76
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Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 136

Qy     146 KAPPPSLPSPSRLPGPSDTPILP 168
           |||||||||||||||||||||||
Db     137 KAPPPSLPSPSRLPGPSDTPILP 159


RESULT 2
Q8WXL2
ID   Q8WXL2      PRELIMINARY;      PRT;   159 AA.
AC   Q8WXL2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397579; AAL69707.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1       1
FT   NON_TER     159     159
SQ   SEQUENCE   159 AA;  16960 MW;  24761E38796A1727 CRC64;

  Query Match             79.6%;  Score 783;  DB 4;  Length 159;
  Best Local Similarity   99.3%;  Pred. No. 5.8e-74;
  Matches  142;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 76

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 136

Qy     146 KAPPPSLPSPSRLPGPSDTPILP 168
           ||||| ||||||||||||||||||
Db     137 KAPPPCLPSPSRLPGPSDTPILP 159


RESULT 3
Q8WXL3
ID   Q8WXL3      PRELIMINARY;      PRT;   159 AA.
AC   Q8WXL3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397578; AAL69706.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1       1
FT   NON_TER     159     159
SQ   SEQUENCE   159 AA;  17006 MW;  AFDC4CE2542EC084 CRC64;

  Query Match             78.9%;  Score 776;  DB 4;  Length 159;
  Best Local Similarity   98.6%;  Pred. No. 3.1e-73;
  Matches  141;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           :| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17 REMLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 76

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 136

Qy     146 KAPPPSLPSPSRLPGPSDTPILP 168
           ||||||||||||||||||||||||
Db     137 KAPPPSLPSPSRLPGPSDTPILP 159


RESULT 4
Q8WXL4
ID   Q8WXL4      PRELIMINARY;      PRT;   159 AA.
AC   Q8WXL4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397576; AAL69704.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1       1
FT   NON_TER     159     159
SQ   SEQUENCE   159 AA;  16909 MW;  A598A73CC97B57EE CRC64;

  Query Match             77.6%;  Score 764;  DB 4;  Length 159;
  Best Local Similarity   97.2%;  Pred. No. 5.6e-72;
  Matches  139;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           :||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17 REPLRPWCHPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 76

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db      77 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQASSSS 136

Qy     146 KAPPPSLPSPSRLPGPSDTPILP 168
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          ||||||||||||||||||||||
Db    137 KAPPPSLPSPSRLPGPSDTPILP 159


RESULT 5
Q8WXL1
ID   Q8WXL1      PRELIMINARY;      PRT;   159 AA.
AC   Q8WXL1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397581; AAL69709.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     159    159
SQ   SEQUENCE   159 AA;  16969 MW;  3C963B3C3D2E57FF CRC64;

  Query Match             77.0%;  Score 758;  DB 4;  Length 159;
  Best Local Similarity   96.5%;  Pred. No. 2.4e-71;
  Matches  138;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           :||||| | |||| ||||||||||||||||||||||||||||||||||||||||||||||
Db      17 REPLRPWCHPINAILAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 76

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db      77 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGTKDHPLTCDDPRFQDSSSS 136

Qy     146 KAPPPSLPSPSRLPGPSDTPILP 168
           ||||||||||||||||||||||||
Db    137 KAPPPSLPSPSRLPGPSDTPILP 159


RESULT 6
Q8WNC5
ID   Q8WNC5      PRELIMINARY;      PRT;   157 AA.
AC   Q8WNC5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397584; AAL69712.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     157    157
SQ   SEQUENCE   157 AA;  17027 MW;  8317774E0F4BD4ED CRC64;

  Query Match             75.0%;  Score 738;  DB 6;  Length 157;
  Best Local Similarity   86.1%;  Pred. No. 2.8e-69;
  Matches  136;  Conservative    4;  Mismatches   12;  Indels    6;  Gaps    1;

Qy       8 LAVVLQRRDWENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTR 67
           | ::   | | :      ||||||||||||||||||||||||:||||||||||||||||
Db       5 LMLLSMGRTWAS------KEPLRPRCRPINATLAVEKEGCPVCVTVNTTICAGYCPTMTR 58

Qy      68 VLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGP 127
           ||| ||| |||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      59 VLQSVLPPLPQVVCNYRDVRFEYIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGP 118

Qy     128 KDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTP 165
           |||||||||||||| |||||||||||||||| || ||
Db     119 KDHPLTCDDPRFQDPSSSKAPPPSLPSPSRLPEPSGTP 156


RESULT 7
Q8WNC4
ID   Q8WNC4      PRELIMINARY;      PRT;   157 AA.
AC   Q8WNC4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397585; AAL69713.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     157    157
SQ   SEQUENCE   157 AA;  16985 MW;  825D27AC3EFBD4F6 CRC64;

  Query Match             74.9%;  Score 737;  DB 6;  Length 157;
  Best Local Similarity   95.0%;  Pred. No. 3.6e-69;
  Matches  133;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           |||||||||||||||||||||||:||||||||||||||||| ||| ||||||||||
Db      17 KEPLRPRCRPINATLAVEKEGCPVCVTVNTTICAGYCPTMTRVLQSVLPPLPQVVCNYRD 76

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||  |||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      77 VRFEYIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDPSSS 136

Qy     146 KAPPPSLPSPSRLPGPSDTP 165
           |||||||||||||| ||:||
Db     137 KAPPPSLPSPSRLPEPSNTP 156


RESULT 8
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```
Q8WNC7
ID   Q8WNC7      PRELIMINARY;      PRT;   157 AA.
AC   Q8WNC7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397582; AAL69710.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     157    157
SQ   SEQUENCE   157 AA;  16928 MW;  825D27A00EFBD4F6 CRC64;

  Query Match            74.7%;  Score 735;  DB 6;  Length 157;
  Best Local Similarity  95.0%;  Pred. No. 5.8e-69;
  Matches  133;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           |||||||||||||||||||||||||:|||||||||||||||||| ||| ||||||||||
Db      17 KEPLRPRCRPINATLAVEKEGCPVCVTVNTTICAGYCPTMTRVLQSVLPPLPQVVCNYRD 76

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      77 VRFEYIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDPSSS 136

Qy     146 KAPPPSLPSPSRLPGPSDTP 165
           ||||||||||||| || ||
Db     137 KAPPPSLPSPSRLPEPSGTP 156


RESULT 9
Q8WNC6
ID   Q8WNC6      PRELIMINARY;      PRT;   157 AA.
AC   Q8WNC6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397583; AAL69711.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     157    157
SQ   SEQUENCE   157 AA;  16868 MW;  97BD27A014E1D4EC CRC64;

  Query Match            73.8%;  Score 726;  DB 6;  Length 157;
  Best Local Similarity  94.3%;  Pred. No. 5.1e-68;
  Matches  132;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           |||||||||||||||||||||||||:|||||||||||||||||| ||| ||||||||||
Db      17 KEPLRPRCRPINATLAVEKEGCPVCVTVNTTICAGYCPTMTRVLQSVLPPLPQVVCNYRD 76

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           |||| ||||||||||||||| ||||||||||||||||||||||||||||||||||| |||
Db      77 VRFEYIRLPGCPRGVNPVVSCAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDPSSS 136

Qy     146 KAPPPSLPSPSRLPGPSDTP 165
           ||||||||||||| || ||
Db     137 KAPPPSLPSPSRLPEPSGTP 156


RESULT 10
Q9BEH1
ID   Q9BEH1      PRELIMINARY;      PRT;   165 AA.
AC   Q9BEH1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Chorionic gonadotropin beta subunit 2.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EMBRYONIC TROPHOBLAST;
RA   Wilken J.A., Matsumoto K., Lasley B.L., Bedows E.;
RT   "A Comparison of Chorionic Gonadotropin Expression by Human and
RT   Macaque Trophoblast Cells.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY026360; AAK08644.1; -.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
SQ   SEQUENCE   165 AA;  17743 MW;  2F21566B48592471 CRC64;

  Query Match            66.8%;  Score 657;  DB 6;  Length 165;
  Best Local Similarity  80.5%;  Pred. No. 8.4e-61;
  Matches  120;  Conservative    7;  Mismatches   22;  Indels    0;  Gaps    0;

Qy      21 GCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVV 80
           | |  :||||| |||||||||| ||| ||||||||||||||||||| |||| ||| :||||
Db      17 GARASREPLRPLCRPINATLAAEKEACPVCITVNTTICAGYCPTMMRVLQAVLPPVPQVV 76

Qy      81 CNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQ 140
           ||||:|||||||||||| ||:||||  ||||||:| ||||||:|||||||||||||  |
Db      77 CNYREVRFESIRLPGCPPGVDPVVSVPVALSCRCGLCRRSTSDCGGPKDHPLTCDDPHLQ 136

Qy     141 DSSSSKAPPPSLPSPSRLPGPSDTPILPQ 169
           ||||| |||| |||||| |:| | |||
Db     137 ASSSSKDPPPSPPSPSRLLEPADNPFLPQ 165


RESULT 11
Q8WNB0
ID   Q8WNB0      PRELIMINARY;      PRT;   159 AA.
AC   Q8WNB0;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
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DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397600; AAL69728.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     159    159
SQ   SEQUENCE   159 AA;  16853 MW;  7B64051C2F863870 CRC64;

  Query Match             66.5%;  Score 654;  DB 6;  Length 159;
  Best Local Similarity   81.1%;  Pred. No. 1.7e-60;
  Matches  120;  Conservative    7;  Mismatches   21;  Indels    0;  Gaps    0;

Qy      21 GCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVV 80
           | |  :|||| |||||||| ||| |||||||||||||||||| |||| ||| :||||
Db      12 GARASREPLRPLCRPINATLAAEKEACPVCITVNTTICAGYCPTMMRVLQAVLPPVPQVV 71

Qy      81 CNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQ 140
           ||||:|||||||||||| ||:|||| |||||:||||||||:|||||||||||||| |
Db      72 CNYREVRFESIRLPGCPPGVDPVVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPHLQ 131

Qy     141 DSSSSKAPPPSLPSPSRLPGPSDTPILP 168
           ||||| |||| |||| |  |:||| ||
Db     132 ASSSSKDPPPSPPSPSGLLEPADTPFLP 159


RESULT 12
Q8WNA9
ID   Q8WNA9      PRELIMINARY;      PRT;   159 AA.
AC   Q8WNA9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397601; AAL69729.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     159    159
SQ   SEQUENCE   159 AA;  16915 MW;  9231691ED0D82863 CRC64;

  Query Match             66.4%;  Score 653;  DB 6;  Length 159;
  Best Local Similarity   80.4%;  Pred. No. 2.1e-60;
  Matches  119;  Conservative    9;  Mismatches   20;  Indels    0;  Gaps    0;

Qy      21 GCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVV 80
           | :  :|||:| ||||||||| ||| |||||||||||||||||| |||| ||| :||||
Db      12 GAQASREPLQPLCRPINATLAAEKEACPVCITVNTTICAGYCPTMMRVLQAVLPPVPQVV 71

Qy      81 CNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQ 140
           ||||:|||||||||||| ||:|||| |||||:||||||||:|||||||||||||| |
Db      72 CNYREVRFESIRLPGCPPGVDPVVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPHLQ 131

Qy     141 DSSSSKAPPPSLPSPSRLPGPSDTPILP 168
           ||||| |||| |||||| |:||| ||
Db     132 ASSSSKDPPPSPPSPSRLLEPADTPFLP 159


RESULT 13
Q9BEH2
ID   Q9BEH2      PRELIMINARY;      PRT;   165 AA.
AC   Q9BEH2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Chorionic gonadotropin beta subunit 1.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EMBRYONIC TROPHOBLAST;
RA   Wilken J.A., Matsumoto K., Lasley B.L., Bedows E.;
RT   "A Comparison of Chorionic Gonadotropin Expression by Human and
RT   Macaque Trophoblast Cells.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY026359; AAK08643.1; -.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
SQ   SEQUENCE   165 AA;  17711 MW;  280DF602157D9940 CRC64;

  Query Match             66.3%;  Score 652;  DB 6;  Length 165;
  Best Local Similarity   79.9%;  Pred. No. 2.8e-60;
  Matches  119;  Conservative    8;  Mismatches   22;  Indels    0;  Gaps    0;

Qy      21 GCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVV 80
           | |  :||||| |||||||| ||| |||||||||||||||||| |||  :|| :||||
Db      17 GARASREPLRPLCRPINATLAAEKEACPVCITVNTTICAGYCPTMMRVLPVILPPVPQVV 76

Qy      81 CNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQ 140
           ||||:|||||||||||| ||:|||| |||||:| ||||||:|||||||||||||| |
Db      77 CNYREVRFESIRLPGCPPGVDPVVSVPVALSCRCGLCRRSTSDCGGPKDHPLTCDDPHLQ 136

Qy     141 DSSSSKAPPPSLPSPSRLPGPSDTPILPQ 169
           ||||| |||| ||||||  |:||| |||
Db     137 ASSSSKDPPPSPPSPSRLLEPADTPFLPQ 165


RESULT 14
Q8WNB2
ID   Q8WNB2      PRELIMINARY;      PRT;   159 AA.
AC   Q8WNB2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
```

```
OS   Colobus guereza (Black-and-white colobus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Colobus.
OX   NCBI_TaxID=33548;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397598; AAL69726.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     159    159
SQ   SEQUENCE   159 AA;  16972 MW;  725BA76BC2887660 CRC64;

  Query Match             65.7%;  Score 646;  DB 6;  Length 159;
  Best Local Similarity   81.8%;  Pred. No. 1.1e-59;
  Matches  117;  Conservative    7;  Mismatches   19;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           :|||||  |||||||||| ||| |||||||||||||||||| |||| ||| :|| |||||:
Db      17 REPLRPLCRPINATLAAEKEACPVCITVNTTICAGYCPTMMRVLQAVLPPVPQAVCNYRE 76

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||| ||:|||| ||||||:| |||||||:||||||||||||||  | ||||
Db      77 VRFESIRLPGCPPGVDPVVSIPVALSCRCGLCRRSTSDCGGPKDHPLTCDDPHLQASSSS 136

Qy     146 KAPPPSLPSPSRLPGPSDTPILP 168
           | ||||||||||| |: || ||
Db     137 KDPPPSLPSPSRLLEPAGTPFLP 159


RESULT 15
Q8WNA8
ID   Q8WNA8      PRELIMINARY;      PRT;   159 AA.
AC   Q8WNA8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397602; AAL69730.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
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FT   NON_TER     159    159
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  Query Match             65.7%;  Score 646;  DB 6;  Length 159;
  Best Local Similarity   80.8%;  Pred. No. 1.1e-59;
  Matches  118;  Conservative    8;  Mismatches   20;  Indels    0;  Gaps    0;

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Db      14 RASREPLRPLCRPINATLAAEKEACPVCITVNTTICAGYCPTMMRVLQVILPPVPQVVCN 73

Qy      83 YRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDS 142
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Qy     143 SSSKAPPPSLPSPSRLPGPSDTPILP 168
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Db     134 SSSKDPPPSPPSPSRLLEPADTPFLP 159


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Job time : 22.8671 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 17:29:06 ; Search time 5.77622 Seconds
(without alignments)
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Title: US-09-787-494-2
Perfect score: 984
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	793	80.6	165	9	US-09-915-676-1	Sequence 1, Appli
2	793	80.6	165	10	US-09-466-320-14	Sequence 14, Appl
3	767	77.9	307	10	US-09-756-186-4	Sequence 4, Appli
4	767	77.9	336	10	US-09-756-186-8	Sequence 8, Appli
5	766	77.8	141	9	US-09-813-398-3	Sequence 3, Appli
6	611	62.1	195	10	US-09-780-933-30	Sequence 30, Appl
7	611	62.1	196	10	US-09-780-933-29	Sequence 29, Appl
8	540	54.9	122	9	US-09-813-398-4	Sequence 4, Appli
9	437	44.4	141	10	US-09-730-617-47	Sequence 47, Appl
10	427	43.4	141	10	US-09-730-617-48	Sequence 48, Appl
11	382	38.8	113	10	US-09-730-617-44	Sequence 44, Appl
12	371	37.7	99	10	US-09-730-617-41	Sequence 41, Appl
13	303	30.8	140	10	US-09-730-617-46	Sequence 46, Appl
14	303	30.8	144	10	US-09-730-617-45	Sequence 45, Appl
15	265.5	27.0	116	10	US-09-730-617-38	Sequence 38, Appl
16	265	26.9	85	10	US-09-730-617-35	Sequence 35, Appl
17	247	25.1	119	9	US-09-813-398-2	Sequence 2, Appli
18	227	23.1	111	9	US-09-973-918A-4	Sequence 4, Appli
19	226	23.0	110	9	US-09-813-398-5	Sequence 5, Appli
20	215	21.8	108	9	US-09-973-918A-11	Sequence 11, Appl
21	215	21.8	109	9	US-09-973-918A-12	Sequence 12, Appl
22	215	21.8	110	9	US-09-973-918A-13	Sequence 13, Appl
23	215	21.8	111	9	US-09-973-918A-6	Sequence 6, Appli
24	215	21.8	111	9	US-09-973-918A-10	Sequence 10, Appl
25	215	21.8	111	10	US-09-780-933-4	Sequence 4, Appli
26	215	21.8	129	10	US-09-780-933-3	Sequence 3, Appli
27	215	21.8	129	10	US-09-780-933-23	Sequence 23, Appl
28	215	21.8	196	10	US-09-780-933-28	Sequence 28, Appl
29	209	21.2	111	9	US-09-973-918A-2	Sequence 2, Appli
30	208	21.1	111	9	US-09-973-918A-8	Sequence 8, Appli
31	204	20.7	38	9	US-09-915-676-3	Sequence 3, Appli
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33	204	20.7	65	10	US-09-466-320-12	Sequence 12, Appl
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36	202	20.5	37	9	US-09-915-676-2	Sequence 2, Appli
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38	143	14.5	106	9	US-09-943-388-9	Sequence 9, Appli
39	143	14.5	106	10	US-09-818-954A-3	Sequence 3, Appli
40	143	14.5	130	9	US-09-943-388-2	Sequence 2, Appli
41	143	14.5	130	9	US-09-943-388-5	Sequence 5, Appli
42	143	14.5	130	10	US-09-818-954A-1	Sequence 1, Appli
43	141	14.3	106	10	US-09-818-954A-13	Sequence 13, Appl
44	141	14.3	130	9	US-09-943-388-23	Sequence 23, Appl
45	141	14.3	130	10	US-09-818-954A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-915-676-1
; Sequence 1, Application US/09915676
; Patent No. US20020164338A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Combined Approach to Treatment of Cancer
; TITLE OF INVENTION: with hCG Vaccines
; FILE REFERENCE: 50450-8027.US01
; CURRENT APPLICATION NUMBER: US/09/915,676
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 09/571,497
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/134,419
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/134,432
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-676-1

Query Match 80.6%; Score 793; DB 9; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3e-57;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
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Db      82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

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RESULT 2
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; Sequence 14, Application US/09466320
; Patent No. US20020025939A1
; GENERAL INFORMATION:
;  APPLICANT: Iversen, Patrick
;  TITLE OF INVENTION: Chorionic Gonadotropin DNA Vaccines and
;  TITLE OF INVENTION: Methods
;  FILE REFERENCE: 0450-0026.30
;  CURRENT APPLICATION NUMBER: US/09/466,320
;  CURRENT FILING DATE: 1999-12-17
;  EARLIER APPLICATION NUMBER: US 60/112,910
;  EARLIER FILING DATE: 1998-12-18
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 165
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: hCG beta sub unit
US-09-466-320-14

  Query Match             80.6%;  Score 793;  DB 10;  Length 165;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-57;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
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Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
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Db     142 KAPPPSLPSPSRLPGPSDTPILPQ 165


RESULT 3
US-09-756-186-4
; Sequence 4, Application US/09756186
; Patent No. US20010014333A1
;  GENERAL INFORMATION:
;    APPLICANT:  Campbell, Robert K.
;    APPLICANT:  Jameson, Bradford A.
;    APPLICANT:  Chappel, Scott C.
;    TITLE OF INVENTION:  HYBRID PROTEINS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street N.W., Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  22207
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/756,186
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/804,166
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Browdy, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  CAMPBELL=2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  307 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-756-186-4

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Db     229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Qy     151 SLPSPSRLPGPSDTPILPQ 169
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Db     289 SLPSPSRLPGPSDTPILPQ 307


RESULT 4
US-09-756-186-8
; Sequence 8, Application US/09756186
; Patent No. US20010014333A1
;  GENERAL INFORMATION:
;    APPLICANT:  Campbell, Robert K.
;    APPLICANT:  Jameson, Bradford A.
;    APPLICANT:  Chappel, Scott C.
;    TITLE OF INVENTION:  HYBRID PROTEINS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street N.W., Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  22207
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/756,186
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/804,166
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Browdy, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  CAMPBELL=2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  336 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-756-186-8
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  Matches  139;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     151 SLPSPSRLPGPSDTPILPQ 169
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Db     318 SLPSPSRLPGPSDTPILPQ 336


RESULT 5
US-09-813-398-3
; Sequence 3, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
;  APPLICANT: Bruce D. Weintraub
;  APPLICANT:  Mariusz W. Szkudlinski
;  APPLICANT:  University of Maryland
;  TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
;  FILE REFERENCE: UOFMD.003C1
;  CURRENT APPLICATION NUMBER: US/09/813,398
;  CURRENT FILING DATE:  2001-03-20
;  PRIOR APPLICATION NUMBER: PCT/US99/05908
;  PRIOR FILING DATE: 1999-03-19
;  PRIOR APPLICATION NUMBER: PCT/US98/19772
;  PRIOR FILING DATE: 1998-09-22
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 141
;   TYPE: PRT
;   ORGANISM: HOMO SAPIEN
US-09-813-398-3

  Query Match             77.8%;  Score 766;  DB 9;  Length 141;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-55;
  Matches  139;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
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Db       3 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 62

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
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Db      63 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 122

Qy     146 KAPPPSLPSPSRLPGPSDT 164
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Db     123 KAPPPSLPSPSRLPGPSDT 141


RESULT 6
US-09-780-933-30
; Sequence 30, Application US/09780933
; Patent No. US20020127652A1
; GENERAL INFORMATION:
;  APPLICANT: SCHAMBYE, HANS T.
;  APPLICANT:  ANDERSEN, KIM V.
;  APPLICANT:  VAN DEN HAZEL, BART
;  APPLICANT:  CHRISTIANSEN, JESPER
;  APPLICANT:  JEPPESENT, CLAUS B.
;  TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
;  FILE REFERENCE: 31-001000US
;  CURRENT APPLICATION NUMBER: US/09/780,933
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: PA 2000 00220
;  PRIOR FILING DATE: 2000-02-11
;  PRIOR APPLICATION NUMBER: 60/184,035
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: PA 2000 01092
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: 60/225,558
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
;   LENGTH: 195
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-780-933-30

  Query Match             62.1%;  Score 611;  DB 10;  Length 195;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-43;
  Matches  110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
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Db      86 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 145

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 135
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Db     146 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 195


RESULT 7
US-09-780-933-29
; Sequence 29, Application US/09780933
; Patent No. US20020127652A1
; GENERAL INFORMATION:
;  APPLICANT: SCHAMBYE, HANS T.
;  APPLICANT:  ANDERSEN, KIM V.
;  APPLICANT:  VAN DEN HAZEL, BART
;  APPLICANT:  CHRISTIANSEN, JESPER
;  APPLICANT:  JEPPESENT, CLAUS B.
;  TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
;  FILE REFERENCE: 31-001000US
;  CURRENT APPLICATION NUMBER: US/09/780,933
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: PA 2000 00220
;  PRIOR FILING DATE: 2000-02-11
;  PRIOR APPLICATION NUMBER: 60/184,035
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: PA 2000 01092
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: 60/225,558
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
;   LENGTH: 196
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-780-933-29

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  Matches  110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
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Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 135
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Db     147 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 196


RESULT 8
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US-09-813-398-4
; Sequence 4, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
;  APPLICANT: Bruce D. Weintraub
;  APPLICANT:  Mariusz W. Szkudlinski
;  APPLICANT:  University of Maryland
;  TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
;  FILE REFERENCE: UOFMD.003C1
;  CURRENT APPLICATION NUMBER: US/09/813,398
;  CURRENT FILING DATE:  2001-03-20
;  PRIOR APPLICATION NUMBER: PCT/US99/05908
;  PRIOR FILING DATE: 1999-03-19
;  PRIOR APPLICATION NUMBER: PCT/US98/19772
;  PRIOR FILING DATE: 1998-09-22
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 122
;   TYPE: PRT
;   ORGANISM: HOMO SAPIEN
US-09-813-398-4

  Query Match             54.9%;  Score 540;  DB 9;  Length 122;
  Best Local Similarity   85.0%;  Pred. No. 2.6e-37;
  Matches   96;  Conservative    6;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           :|||||  | ||||  ||||||||||||||||||||||||||||| |||| ||| ||||||  |||
Db       3 REPLRPWCHPINAILAVEKEGCPVCITVNTTICAGYCPTMMRVLQAVLPPLPQVVCTYRD 62

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPR 138
           ||||||||||||||||:||||: |||||:|  |||||:||||||||||||| |:
Db      63 VRFESIRLPGCPRGVDPVVSFPVALSCRCGPCRRRSTSDCGGPKDHPLTCDHPQ 115


RESULT 9
US-09-730-617-47
; Sequence 47, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
;  APPLICANT: Burgess, Catherine E
;  APPLICANT:  Prayaga, Sudhirdas K
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Zerhusen, Bryan D
;  APPLICANT:  Mezes, Peter S
;  TITLE OF INVENTION: No. US20020068279A1el Proteins and Nucleic Acids Encoding the Sam
;  FILE REFERENCE: 15966-609
;  CURRENT APPLICATION NUMBER: US/09/730,617
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: 60/169,056
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: 60/169,886
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/169,866
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/170,252
;  PRIOR FILING DATE: 1999-12-10
;  PRIOR APPLICATION NUMBER: 60/175,740
;  PRIOR FILING DATE: 2000-01-12
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
;   LENGTH: 141
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-09-730-617-47

  Query Match             44.4%;  Score 437;  DB 10;  Length 141;
  Best Local Similarity   61.6%;  Pred. No. 6.3e-29;
  Matches   77;  Conservative   14;  Mismatches   28;  Indels    6;  Gaps    1;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| |:|||||| ||| ||||||  |:|||||||:| |||  :|| :
Db      19 WASRG------PLRPLCQPINATLAAEKEACPVCITFTTSICAGYCPSMKRVLPVILPPM 72

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
           || || | ::|| |:|||||| ||:|:||: ||||| |  || |:||||||:  || ||
Db      73 PQRVCTYHELRFASVRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDH 132

Qy     137 PRFQD 141
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Db     133 PPLPD 137


RESULT 10
US-09-730-617-48
; Sequence 48, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
;  APPLICANT: Burgess, Catherine E
;  APPLICANT:  Prayaga, Sudhirdas K
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Zerhusen, Bryan D
;  APPLICANT:  Mezes, Peter S
;  TITLE OF INVENTION: No. US20020068279A1el Proteins and Nucleic Acids Encoding the
;  FILE REFERENCE: 15966-609
;  CURRENT APPLICATION NUMBER: US/09/730,617
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: 60/169,056
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: 60/169,886
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/169,866
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/170,252
;  PRIOR FILING DATE: 1999-12-10
;  PRIOR APPLICATION NUMBER: 60/175,740
;  PRIOR FILING DATE: 2000-01-12
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
;   LENGTH: 141
;   TYPE: PRT
;   ORGANISM: Ovis aries
US-09-730-617-48

  Query Match             43.4%;  Score 427;  DB 10;  Length 141;
  Best Local Similarity   60.8%;  Pred. No. 4e-28;
  Matches   76;  Conservative   14;  Mismatches   29;  Indels    6;  Gaps    1;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| |:|||||| ||| ||||||  |:|||||| :| |||  :|| :
Db      19 WASRG------PLRPLCQPINATLAAEKEACPVCITFTTSICAGYCLSMKRVLPVILPPM 72

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDD 136
           || || | ::|| |:|||||| ||:|:||: ||||| |  || |:||||||:  || ||
Db      73 PQRVCTYHELRFASVRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDH 132

Qy     137 PRFQD 141
           |   |
Db     133 PPLPD 137


RESULT 11
US-09-730-617-44
; Sequence 44, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
;  APPLICANT: Burgess, Catherine E
;  APPLICANT:  Prayaga, Sudhirdas K
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Zerhusen, Bryan D
```

```
;  APPLICANT:  Mezes, Peter S
;  TITLE OF INVENTION: No. US20020068279Alel Proteins and Nucleic Acids Encoding the Sam
;  FILE REFERENCE: 15966-609
;  CURRENT APPLICATION NUMBER: US/09/730,617
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: 60/169,056
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: 60/169,886
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/169,866
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/170,252
;  PRIOR FILING DATE: 1999-12-10
;  PRIOR APPLICATION NUMBER: 60/175,740
;  PRIOR FILING DATE: 2000-01-12
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
;   LENGTH: 113
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-730-617-44

  Query Match             38.8%;  Score 382;  DB 10;  Length 113;
  Best Local Similarity   63.6%;  Pred. No. 1.4e-24;
  Matches   68;  Conservative   12;  Mismatches   21;  Indels    6;  Gaps    1;

Qy      17 WENPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPAL 76
           | : |      |||| ||||||||| ||| ||:||| |:||||||:| ||:   |||:
Db      13 WASRG------PLRPLCRPINATLAAEKEACPICITFTTSICAGYCPSMVRVMPAALPAI 66

Qy      77 PQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTD 123
           || || ||::|| |||||||| ||:|:||: ||||| |  |:  |||
Db      67 PQPVCTYRELRFASIRLPGCPPGVDPMVSFPVALSCHCGPCQIKTTD 113


RESULT 12
US-09-730-617-41
; Sequence 41, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
;  APPLICANT: Burgess, Catherine E
;  APPLICANT:  Prayaga, Sudhirdas K
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Zerhusen, Bryan D
;  APPLICANT:  Mezes, Peter S
;  TITLE OF INVENTION: No. US20020068279Alel Proteins and Nucleic Acids Encoding the Sam
;  FILE REFERENCE: 15966-609
;  CURRENT APPLICATION NUMBER: US/09/730,617
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: 60/169,056
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: 60/169,886
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/169,866
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/170,252
;  PRIOR FILING DATE: 1999-12-10
;  PRIOR APPLICATION NUMBER: 60/175,740
;  PRIOR FILING DATE: 2000-01-12
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
;   LENGTH: 99
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-730-617-41

  Query Match             37.7%;  Score 371;  DB 10;  Length 99;
  Best Local Similarity   67.7%;  Pred. No. 9.2e-24;
  Matches   65;  Conservative   12;  Mismatches   19;  Indels    0;  Gaps    0;

Qy      28 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 87
           |||| |:||||||| ||| |||||| |:||||||:| |||  :|| :|| || | ::|
Db       4 PLRPLCQPINATLAAEKEACPVCITFTTSICAGYCPSMKRVLPVILPPMPQRVCTYHELR 63

Qy      88 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTD 123
           | |:|||||| ||:|:||: ||||| |  || |:||
Db      64 FASVRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTD 99


RESULT 13
US-09-730-617-46
; Sequence 46, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
;  APPLICANT: Burgess, Catherine E
;  APPLICANT:  Prayaga, Sudhirdas K
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Zerhusen, Bryan D
;  APPLICANT:  Mezes, Peter S
;  TITLE OF INVENTION: No. US20020068279Alel Proteins and Nucleic Acids Encoding the
;  FILE REFERENCE: 15966-609
;  CURRENT APPLICATION NUMBER: US/09/730,617
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: 60/169,056
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: 60/169,886
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/169,866
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/170,252
;  PRIOR FILING DATE: 1999-12-10
;  PRIOR APPLICATION NUMBER: 60/175,740
;  PRIOR FILING DATE: 2000-01-12
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
;   LENGTH: 140
;   TYPE: PRT
;   ORGANISM: Carassius auratus
US-09-730-617-46

  Query Match             30.8%;  Score 303;  DB 10;  Length 140;
  Best Local Similarity   54.3%;  Pred. No. 4.2e-18;
  Matches   51;  Conservative   16;  Mismatches   27;  Indels    0;  Gaps    0;

Qy      31 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 90
           | | |:| |:|||||||| |: : ||||:|:| |   | :     : | || |||||:|:
Db      27 PPCEPVNETVAVEKEGCPKCLVLQTTICSGHCLTKEPVYKSPFSTVYQHVCTYRDVRYET 86

Qy      91 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 124
           :||| || ||:| ::| |||||  |:||   |:||
Db      87 VRLPDCPPGVDPHITYPVALSCDCSLCTMDTSDC 120


RESULT 14
US-09-730-617-45
; Sequence 45, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
;  APPLICANT: Burgess, Catherine E
;  APPLICANT:  Prayaga, Sudhirdas K
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Zerhusen, Bryan D
;  APPLICANT:  Mezes, Peter S
;  TITLE OF INVENTION: No. US20020068279Alel Proteins and Nucleic Acids Encoding the
;  FILE REFERENCE: 15966-609
;  CURRENT APPLICATION NUMBER: US/09/730,617
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: 60/169,056
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: 60/169,886
```

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;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/169,866
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/170,252
;  PRIOR FILING DATE: 1999-12-10
;  PRIOR APPLICATION NUMBER: 60/175,740
;  PRIOR FILING DATE: 2000-01-12
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
;   LENGTH: 144
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-730-617-45

  Query Match             30.8%;  Score 303;  DB 10;  Length 144;
  Best Local Similarity   54.3%;  Pred. No. 4.3e-18;
  Matches   51;  Conservative   16;  Mismatches   27;  Indels    0;  Gaps    0;

Qy      31 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 90
           | | |:| |:||||||||| |: : ||||:|:| |   | :     : | || |||||:|:
Db      31 PPCEPVNETVAVEKEGCPKCLVLQTTICSGHCLTKEPVYKSPFSTVYQHVCTYRDVRYET 90

Qy      91 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 124
           :||| || ||:| ::| ||||| |:||   |:||
Db      91 VRLPDCPPGVDPHITYPVALSCDCSLCTMDTSDC 124


RESULT 15
US-09-730-617-38
; Sequence 38, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
;  APPLICANT: Burgess, Catherine E
;  APPLICANT:  Prayaga, Sudhirdas K
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Zerhusen, Bryan D
;  APPLICANT:  Mezes, Peter S
;  TITLE OF INVENTION: No. US20020068279A1el Proteins and Nucleic Acids Encoding the Sam
;  FILE REFERENCE: 15966-609
;  CURRENT APPLICATION NUMBER: US/09/730,617
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: 60/169,056
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: 60/169,886
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/169,866
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/170,252
;  PRIOR FILING DATE: 1999-12-10
;  PRIOR APPLICATION NUMBER: 60/175,740
;  PRIOR FILING DATE: 2000-01-12
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-730-617-38

  Query Match             27.0%;  Score 265.5;  DB 10;  Length 116;
  Best Local Similarity   50.5%;  Pred. No. 3.6e-15;
  Matches   48;  Conservative   18;  Mismatches   28;  Indels    1;  Gaps    1;

Qy      29 LRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRF 88
           |:| |  :| |::||||||| |:   ||||:|:|||   | :     : | || | : |:
Db      23 LQP-CVLVNETVSVEKEGCPRCLVFRTTICSGHCPTKEPVYKSPFSVVNQHVCTYGNFRY 81

Qy      89 ESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTD 123
           |:|||| |  ||:|:|:| |||||:|:||   |:|
Db      82 ETIRLPDCADGVDPLVTYPVALSCECSLCSMDTSD 116


Search completed: November 20, 2002, 17:35:34
Job time : 6.77622 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:27 ; Search time 10.7273 Seconds
(without alignments)
485.478 Million cell updates/sec

Title: US-09-787-494-2
Perfect score: 984
Sequence: 1 MTMITDSLAVVLQRRDWENP.....LPGPSDTPILPQTSHHHHHH 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	795	80.8	265	4	US-08-918-288-3	Sequence 3, Appli
2	795	80.8	265	4	US-08-918-288-39	Sequence 39, Appl
3	795	80.8	265	4	US-09-282-357-3	Sequence 3, Appli
4	795	80.8	265	4	US-09-282-357-39	Sequence 39, Appl
5	793	80.6	145	1	US-08-475-213-10	Sequence 10, Appl
6	793	80.6	145	2	US-08-395-238-2	Sequence 2, Appli
7	793	80.6	145	4	US-09-142-320-12	Sequence 12, Appl
8	793	80.6	145	4	US-09-142-320-13	Sequence 13, Appl
9	793	80.6	145	4	US-09-142-320-14	Sequence 14, Appl
10	793	80.6	145	4	US-09-142-320-15	Sequence 15, Appl
11	793	80.6	145	4	US-08-918-288-68	Sequence 68, Appl
12	793	80.6	145	4	US-09-282-357-68	Sequence 68, Appl
13	793	80.6	145	4	US-08-908-371B-1	Sequence 1, Appli
14	790	80.3	165	2	US-08-709-924-2	Sequence 2, Appli
15	790	80.3	165	2	US-08-709-925-2	Sequence 2, Appli
16	790	80.3	165	4	US-08-709-948-2	Sequence 2, Appli
17	789	80.2	181	4	US-08-918-288-36	Sequence 36, Appl
18	789	80.2	181	4	US-09-282-357-36	Sequence 36, Appl
19	787	80.0	145	1	US-08-425-673-1	Sequence 1, Appli
20	787	80.0	145	1	US-08-425-673-2	Sequence 2, Appli
21	787	80.0	145	1	US-08-298-189B-1	Sequence 1, Appli
22	785	79.8	145	4	US-09-142-320-16	Sequence 16, Appl
23	773	78.6	145	4	US-09-142-320-11	Sequence 11, Appl
24	772	78.5	145	4	US-09-142-320-4	Sequence 4, Appli
25	767	77.9	307	4	US-08-804-166-4	Sequence 4, Appli
26	767	77.9	307	4	US-08-910-991-4	Sequence 4, Appli
27	767	77.9	336	4	US-08-804-166-8	Sequence 8, Appli
28	767	77.9	336	4	US-08-910-991-8	Sequence 8, Appli
29	766	77.8	145	1	US-08-425-673-10	Sequence 10, Appl
30	644	65.4	234	4	US-08-918-288-6	Sequence 6, Appli
31	644	65.4	234	4	US-09-282-357-6	Sequence 6, Appli
32	629	63.9	114	4	US-08-918-288-69	Sequence 69, Appl
33	629	63.9	114	4	US-09-282-357-69	Sequence 69, Appl
34	578	58.7	234	4	US-08-918-288-24	Sequence 24, Appl
35	578	58.7	234	4	US-09-282-357-24	Sequence 24, Appl
36	565	57.4	114	1	US-08-425-673-9	Sequence 9, Appli
37	557	56.6	114	1	US-08-425-673-7	Sequence 7, Appli
38	555	56.4	234	4	US-08-918-288-9	Sequence 9, Appli
39	555	56.4	234	4	US-09-282-357-9	Sequence 9, Appli
40	549	55.8	234	4	US-08-918-288-21	Sequence 21, Appl
41	549	55.8	234	4	US-09-282-357-21	Sequence 21, Appl
42	545	55.4	237	4	US-08-918-288-18	Sequence 18, Appl
43	545	55.4	237	4	US-09-282-357-18	Sequence 18, Appl
44	540	54.9	114	4	US-08-918-288-71	Sequence 71, Appl
45	540	54.9	114	4	US-09-282-357-71	Sequence 71, Appl

ALIGNMENTS

```
RESULT 1
US-08-918-288-3
; Sequence 3, Application US/08918288
; Patent No. 6238890
;  GENERAL INFORMATION:
;    APPLICANT:  BOIME, Irving
;    APPLICANT:  MOYLE, William R.
;    TITLE OF INVENTION:  SINGLE-CHAIN FORMS OF THE
;    TITLE OF INVENTION:  GLYCOPROTEIN HORMONE QUARTET
;    NUMBER OF SEQUENCES:  83
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/918,288
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/282,357
;      FILING DATE:
;      APPLICATION NUMBER:  08/853,524
;      FILING DATE:  09-MAY-1997
;      APPLICATION NUMBER:  08/199,382
;      FILING DATE:  18-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  29500-20050.25
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-887-0763
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  265 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-918-288-3
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  Query Match             80.8%;  Score 795;  DB 4;  Length 265;
  Best Local Similarity   99.3%;  Pred. No. 2.3e-64;
  Matches  145;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
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Db      22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQTS 171
           ||||||||||||||||||||||| |
Db     142 KAPPPSLPSPSRLPGPSDTPILPQGS 167


RESULT 2
US-08-918-288-39
; Sequence 39, Application US/08918288
; Patent No. 6238890
;  GENERAL INFORMATION:
;    APPLICANT:  BOIME, Irving
;    APPLICANT:  MOYLE, William R.
;    TITLE OF INVENTION:  SINGLE-CHAIN FORMS OF THE
;    TITLE OF INVENTION:  GLYCOPROTEIN HORMONE QUARTET
;    NUMBER OF SEQUENCES:  83
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/918,288
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/282,357
;      FILING DATE:
;      APPLICATION NUMBER:  08/853,524
;      FILING DATE:  09-MAY-1997
;      APPLICATION NUMBER:  08/199,382
;      FILING DATE:  18-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  29500-20050.25
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-887-0763
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  265 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-918-288-39

  Query Match             80.8%;  Score 795;  DB 4;  Length 265;
  Best Local Similarity   99.3%;  Pred. No. 2.3e-64;
  Matches  145;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQTS 171
           ||||||||||||||||||||||| |
Db     142 KAPPPSLPSPSRLPGPSDTPILPQGS 167


RESULT 3
US-09-282-357-3
; Sequence 3, Application US/09282357
; Patent No. 6242580
;  GENERAL INFORMATION:
;    APPLICANT:  BOIME, Irving
;    APPLICANT:  MOYLE, William R.
;    TITLE OF INVENTION:  SINGLE-CHAIN FORMS OF THE
;    TITLE OF INVENTION:  GLYCOPROTEIN HORMONE QUARTET
;    NUMBER OF SEQUENCES:  83
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/282,357
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/918,288
;      FILING DATE:  25 AUG-1997
;      APPLICATION NUMBER:  08/853,524
;      FILING DATE:  09-MAY-1997
;      APPLICATION NUMBER:  08/199,382
;      FILING DATE:  18-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  29500-20050.25
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-887-0763
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  265 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-09-282-357-3

  Query Match             80.8%;  Score 795;  DB 4;  Length 265;
  Best Local Similarity   99.3%;  Pred. No. 2.3e-64;
  Matches  145;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy    146 KAPPPSLPSPSRLPGPSDTPILPQTS 171
          |||||||||||||||||||||||||| |
Db    142 KAPPPSLPSPSRLPGPSDTPILPQGS 167


RESULT 4
US-09-282-357-39
; Sequence 39, Application US/09282357
; Patent No. 6242580
;  GENERAL INFORMATION:
;    APPLICANT:  BOIME, Irving
;    APPLICANT:  MOYLE, William R.
;    TITLE OF INVENTION:  SINGLE-CHAIN FORMS OF THE
;    TITLE OF INVENTION:  GLYCOPROTEIN HORMONE QUARTET
;    NUMBER OF SEQUENCES:  83
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/282,357
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/918,288
;      FILING DATE:  25 AUG-1997
;      APPLICATION NUMBER:  08/853,524
;      FILING DATE:  09-MAY-1997
;      APPLICATION NUMBER:  08/199,382
;      FILING DATE:  18-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  29500-20050.25
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-887-0763
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  265 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-09-282-357-39

  Query Match             80.8%;  Score 795;  DB 4;  Length 265;
  Best Local Similarity   99.3%;  Pred. No. 2.3e-64;
  Matches  145;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy     86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy    146 KAPPPSLPSPSRLPGPSDTPILPQTS 171
          |||||||||||||||||||||||||| |
Db    142 KAPPPSLPSPSRLPGPSDTPILPQGS 167


RESULT 5
US-08-475-213-10
; Sequence 10, Application US/08475213
; Patent No. 5783674
;  GENERAL INFORMATION:
;    APPLICANT:  Geysen, Hendrik M.
;    TITLE OF INVENTION:  Method for the use and Synthesis of
;    TITLE OF INVENTION:  Peptides
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Chiron Corporation
;      STREET:  4560 Horton Street
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94608
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,213
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/752,437
;      FILING DATE:  06-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO pct/au90/00062
;      FILING DATE:  16-FEB-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PJ2788/89
;      FILING DATE:  17-FEB-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Green, Grant D.
;      REGISTRATION NUMBER:  31259
;      REFERENCE/DOCKET NUMBER:  0240.002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-601-2706
;      TELEFAX:  510-655-3542
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  145 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-475-213-10

  Query Match             80.6%;  Score 793;  DB 1;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-64;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy     86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy    146 KAPPPSLPSPSRLPGPSDTPILPQ 169
          ||||||||||||||||||||||||
Db    122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 6
US-08-395-238-2
; Sequence 2, Application US/08395238
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; Patent No. 5864488
;  GENERAL INFORMATION:
;    APPLICANT:  ISSACS, Neil William
;    APPLICANT:  LAPTHORN, Adrian Jonathan
;    APPLICANT:  HARRIS, Deborah Claire
;    TITLE OF INVENTION:  THREE DIMENSIONAL HORMONE STRUCTURE
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AKZO NOBEL PATENT DEPARTMENT
;      STREET:  1300 PICCARD DRIVE, SUITE 206
;      CITY:  ROCKVILLE
;      STATE:  MARYLAND
;      COUNTRY:  UNITED STATES
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/395,238
;      FILING DATE:  24-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9403600.1
;      FILING DATE:  24-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WILLIAM M. BLACKSTONE
;      REGISTRATION NUMBER:  29,722
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  145 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      STRAIN:  BETA-SUBUNIT HUMAN CHORIONIC GONADOTROPIN
US-08-395-238-2

  Query Match             80.6%;  Score 793;  DB 2;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-64;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
           |||||||||||||||||||||||||
Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 7
US-09-142-320-12
; Sequence 12, Application US/09142320
; Patent No. 6194154
; GENERAL INFORMATION:
;  APPLICANT: Bellet, Dominique
;  APPLICANT: Bidart, Jean-Michel
;  APPLICANT: Vidaud, Michel
;  APPLICANT: Lazar, Vladimir
;  TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION  DETECTION METHOD
;  FILE REFERENCE: 065691/0140
;  CURRENT APPLICATION NUMBER: US/09/142,320
;  CURRENT FILING DATE: 1998-09-04
;  EARLIER APPLICATION NUMBER: PCT/FR97/00361
;  EARLIER FILING DATE: 1997-02-28
;  EARLIER APPLICATION NUMBER: FR 96 02683
;  EARLIER FILING DATE: 1996-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 145
;   TYPE: PRT
;   ORGANISM: human
US-09-142-320-12

  Query Match             80.6%;  Score 793;  DB 4;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-64;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
           |||||||||||||||||||||||||
Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 8
US-09-142-320-13
; Sequence 13, Application US/09142320
; Patent No. 6194154
; GENERAL INFORMATION:
;  APPLICANT: Bellet, Dominique
;  APPLICANT: Bidart, Jean-Michel
;  APPLICANT: Vidaud, Michel
;  APPLICANT: Lazar, Vladimir
;  TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION  DETECTION METHOD
;  FILE REFERENCE: 065691/0140
;  CURRENT APPLICATION NUMBER: US/09/142,320
;  CURRENT FILING DATE: 1998-09-04
;  EARLIER APPLICATION NUMBER: PCT/FR97/00361
;  EARLIER FILING DATE: 1997-02-28
;  EARLIER APPLICATION NUMBER: FR 96 02683
;  EARLIER FILING DATE: 1996-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 145
;   TYPE: PRT
;   ORGANISM: human
US-09-142-320-13

  Query Match             80.6%;  Score 793;  DB 4;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-64;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
           |||||||||||||||||||||||||
Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 9
US-09-142-320-14
; Sequence 14, Application US/09142320
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; Patent No. 6194154
; GENERAL INFORMATION:
;  APPLICANT: Bellet, Dominique
;  APPLICANT: Bidart, Jean-Michel
;  APPLICANT: Vidaud, Michel
;  APPLICANT: Lazar, Vladimir
;  TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION  DETECTION METHOD
;  FILE REFERENCE: 065691/0140
;  CURRENT APPLICATION NUMBER: US/09/142,320
;  CURRENT FILING DATE: 1998-09-04
;  EARLIER APPLICATION NUMBER: PCT/FR97/00361
;  EARLIER FILING DATE: 1997-02-28
;  EARLIER APPLICATION NUMBER: FR 96 02683
;  EARLIER FILING DATE: 1996-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 145
;   TYPE: PRT
;   ORGANISM: human
US-09-142-320-14

  Query Match             80.6%;  Score 793;  DB 4;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-64;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
           |||||||||||||||||||||||||
Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 10
US-09-142-320-15
; Sequence 15, Application US/09142320
; Patent No. 6194154
; GENERAL INFORMATION:
;  APPLICANT: Bellet, Dominique
;  APPLICANT: Bidart, Jean-Michel
;  APPLICANT: Vidaud, Michel
;  APPLICANT: Lazar, Vladimir
;  TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION  DETECTION METHOD
;  FILE REFERENCE: 065691/0140
;  CURRENT APPLICATION NUMBER: US/09/142,320
;  CURRENT FILING DATE: 1998-09-04
;  EARLIER APPLICATION NUMBER: PCT/FR97/00361
;  EARLIER FILING DATE: 1997-02-28
;  EARLIER APPLICATION NUMBER: FR 96 02683
;  EARLIER FILING DATE: 1996-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 145
;   TYPE: PRT
;   ORGANISM: human
US-09-142-320-15

  Query Match             80.6%;  Score 793;  DB 4;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-64;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
           |||||||||||||||||||||||||
Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 11
US-08-918-288-68
; Sequence 68, Application US/08918288
; Patent No. 6238890
;  GENERAL INFORMATION:
;    APPLICANT:  BOIME, Irving
;    APPLICANT:  MOYLE, William R.
;    TITLE OF INVENTION:  SINGLE-CHAIN FORMS OF THE
;    TITLE OF INVENTION:  GLYCOPROTEIN HORMONE QUARTET
;    NUMBER OF SEQUENCES:  83
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/918,288
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/282,357
;      FILING DATE:
;      APPLICATION NUMBER:  08/853,524
;      FILING DATE:  09-MAY-1997
;      APPLICATION NUMBER:  08/199,382
;      FILING DATE:  18-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  29500-20050.25
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-887-0763
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  145 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-918-288-68

  Query Match             80.6%;  Score 793;  DB 4;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-64;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
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Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
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Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145
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RESULT 12
US-09-282-357-68
; Sequence 68, Application US/09282357
; Patent No. 6242580
;  GENERAL INFORMATION:
;    APPLICANT:  BOIME, Irving
;    APPLICANT:  MOYLE, William R.
;    TITLE OF INVENTION:  SINGLE-CHAIN FORMS OF THE
;    TITLE OF INVENTION:  GLYCOPROTEIN HORMONE QUARTET
;    NUMBER OF SEQUENCES:  83
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/282,357
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/918,288
;      FILING DATE:  25 AUG-1997
;      APPLICATION NUMBER:  08/853,524
;      FILING DATE:  09-MAY-1997
;      APPLICATION NUMBER:  08/199,382
;      FILING DATE:  18-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  29500-20050.25
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-887-0763
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  145 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-282-357-68

  Query Match           80.6%;  Score 793;  DB 4;  Length 145;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-64;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
           |||||||||||||||||||||||||
Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 13
US-08-908-371B-1
; Sequence 1, Application US/08908371B
; Patent No. 6331610
;  GENERAL INFORMATION:
;    APPLICANT: •Bourinbaiar, Aldar S.
;    TITLE OF INVENTION:  A Method for Preventing and Treating
;    TITLE OF INVENTION:  AIDS and HIV Infection Using Select Peptides From the
;    TITLE OF INVENTION:  Beta Subunit of Human Chorionic Gonadotropin
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Metatron, Inc.
;      STREET:  367 Bay Shore Road
;      CITY:  Deer Park
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  11729
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 in. diskette (1.44megabytes)
;      COMPUTER:  IBM Compatible PC
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WORD 6.0  ASCII TEXT CONVERSION ONLY
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/908,371B
;      FILING DATE:  07-AUG-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/044,937
;      FILING DATE:  25-APR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COLEMAN, HENRY D.
;      REGISTRATION NUMBER:  32,559
;      REFERENCE/DOCKET NUMBER:  M31-013
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 679-0090
;      TELEFAX:  (212) 679-9121
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  145 Amino Acid Units
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Single Stranded
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  Protein Subunit
;      DESCRIPTION:  Amino Acid Corresponding to Beta Subunit
;      DESCRIPTION:  of Human Chorionic Gonadotropin
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:  Sequence
;    IMMEDIATE SOURCE:  N/A
;    POSITION IN GENOME:  N/A
;    FEATURE:
;      NAME/KEY:  145 Units of Beta Subunit of Human Chorionic
;      NAME/KEY:  Gonadotropin
;      LOCATION:  N/A
;      IDENTIFICATION METHOD:  Sequencing
;    PUBLICATION INFORMATION:
;      AUTHORS:  CARLSEN, Robert B.,
;      AUTHORS:  BAHL, Ohm P.
;      AUTHORS:  SWAMINATHAN, N.
;      TITLE:  HUMAN CHORIONIC GONADOTROPIN
;      JOURNAL:  THE JOURNAL OF BIOLOGICAL CHEMISTRY
;      VOLUME:  248
;      PAGES:  6810-6825
;      DATE:  1973
US-08-908-371B-1

  Query Match           80.6%;  Score 793;  DB 4;  Length 145;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-64;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
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Db    122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 14
US-08-709-924-2
; Sequence 2, Application US/08709924
; Patent No. 5968513
;  GENERAL INFORMATION:
;    APPLICANT:  Gallo, Robert C.
;    APPLICANT:  Bryant, Joseph
;    APPLICANT:  Lunardi-Iskandar, Yanto
;    TITLE OF INVENTION:  METHODS OF PROMOTING HEMATOPOIESIS
;    TITLE OF INVENTION:  USING DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,924
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  8769-018
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  165 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-709-924-2

  Query Match             80.3%;  Score 790;  DB 2;  Length 165;
  Best Local Similarity   99.3%;  Pred. No. 3.8e-64;
  Matches  143;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
           |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db      82 VRFESIRLPGCPRGLNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
           ||||||||||||||||||||||||
Db     142 KAPPPSLPSPSRLPGPSDTPILPQ 165


RESULT 15
US-08-709-925-2
; Sequence 2, Application US/08709925
; Patent No. 5997871
;  GENERAL INFORMATION:
;    APPLICANT:  Gallo, Robert C.
;    APPLICANT:  Bryant, Joseph
;    APPLICANT:  Lunardi-Iskandar, Yanto
;    TITLE OF INVENTION:  TREATMENT AND PREVENTION OF CANCER BY
;    TITLE OF INVENTION:  ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROP
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,925
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  512
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  8769-017
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  165 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-709-925-2

  Query Match             80.3%;  Score 790;  DB 2;  Length 165;
  Best Local Similarity   99.3%;  Pred. No. 3.8e-64;
  Matches  143;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      26 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 85
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      86 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 145
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Db      82 VRFESIRLPGCPRGLNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy     146 KAPPPSLPSPSRLPGPSDTPILPQ 169
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Db     142 KAPPPSLPSPSRLPGPSDTPILPQ 165


Search completed: November 20, 2002, 17:29:32
Job time : 11.7273 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:27 ; Search time 17.035 Seconds
(without alignments)
1422.126 Million cell updates/sec

Title: US-09-787-494-4
Perfect score: 1347
Sequence: 1 MRFPSIFTAVLFAASSALAA.....LPGPSDTPILPQTSHHHHHH 252

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	793	58.9	165	1	KTHUB	choriogonadotropin
2	785	58.3	145	2	I37231	beta-gonadotropin
3	651	48.3	165	1	KTBAB	choriogonadotropin
4	540	40.1	141	1	UTHUB	lutropin beta chai
5	444	33.0	169	1	KTHOB	choriogonadotropin
6	435	32.3	141	1	UTBOB	lutropin beta chai
7	435	32.3	141	1	UTSHB	lutropin beta chai
8	432	32.1	141	1	UTRTB	lutropin beta chai
9	431	32.0	139	2	I52320	testicular luteini
10	429.5	31.9	165	1	JFBY1	mating pheromone a
11	427	31.7	119	2	A61465	lutropin beta chai
12	425	31.6	141	1	UTPGB	lutropin beta chai
13	421	31.3	141	2	JC4527	luteinizing hormon
14	418	31.0	138	2	S00512	lutropin beta chai
15	407	30.2	118	2	PN0139	lutropin beta chai
16	406	30.1	118	2	PN0141	lutropin beta chai
17	303	22.5	144	1	UTCAB	gonadotropin beta
18	301	22.3	141	1	B60626	gonadotropin beta
19	301	22.3	146	1	S16763	gonadotropin beta
20	291	21.6	142	1	C36179	gonadotropin II be
21	288	21.4	142	2	I51232	gonadotropin II be
22	278	20.6	142	1	A25800	gonadotropin beta
23	276.5	20.5	113	1	S07092	gonadotropin beta
24	273	20.3	140	2	A48166	gonadotropin II be
25	273	20.3	142	2	I50143	gonadotropin II be
26	269	20.0	128	2	S74085	lutropin beta chai
27	269	20.0	158	2	A61091	lutropin beta chai
28	265	19.7	112	2	S21196	lutropin beta chai
29	260	19.3	159	2	I51373	luteinizing hormon
30	258	19.2	166	2	I51242	luteinizing hormon
31	255.5	19.0	80	2	I65235	testicular luteini
32	255	18.9	147	2	I50994	gonadotropin II be
33	243	18.0	138	1	TTHUB	thyrotropin beta c
34	243	18.0	138	1	TTBOB	thyrotropin beta c
35	242	18.0	138	1	TTPGB	thyrotropin beta c
36	240	17.8	138	2	A29479	thyrotropin beta c
37	239	17.7	138	1	TTRTB	thyrotropin beta c
38	229	17.0	136	2	I50554	gonadotropin II be
39	227	16.9	118	1	FTHOB	follitropin beta c
40	226	16.8	120	2	S05791	mating pheromone a
41	222	16.5	130	2	JC4526	follitropin beta c
42	218	16.2	130	2	A32893	follitropin beta c
43	215	16.0	129	1	FTHUB	follitropin beta c
44	215	16.0	129	1	FTSHB	follitropin beta c
45	209	15.5	129	2	A23550	follitropin beta c

ALIGNMENTS

RESULT 1
KTHUB
choriogonadotropin beta chain precursor [validated] - human
N;Alternate names: beta-gonadotropin; chorionic gonadotropin beta chain
C;Species: Homo sapiens (man)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 08-Dec-2000
C;Accession: A93230; I69972; I55224; I55250; I70007; I70008; A92303; A92181; A92142;
R;Fiddes, J.C.; Goodman, H.M.
Nature 286, 684-687, 1980
A;Title: The cDNA for the beta-subunit of human chorionic gonadotropin suggests evolu
A;Reference number: A93230; MUID:81012134; PMID:6774259
A;Accession: A93230
A;Molecule type: mRNA
A;Residues: 1-165 <FID>
A;Cross-references: GB:J00117; GB:M38559; GB:M54963; NID:g180436; PIDN:AAA96690.1; PI
R;Policastro, P.; Ovitt, C.E.; Hoshina, M.; Fukuoka, H.; Boothby, M.R.; Boime, I.
J. Biol. Chem. 258, 11492-11499, 1983
A;Title: The beta subunit of human chorionic gonadotropin is encoded by multiple gene
A;Reference number: I55224; MUID:84008141; PMID:6194155
A;Accession: I69972
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-165 <POL>
A;Cross-references: GB:K03189; NID:g180450; PIDN:AAA53288.1; PID:g180453
A;Note: clone CG-beta-e
A;Accession: I55224
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-23,'M',25-136,'A',138-165 <PO2>
A;Cross-references: GB:K03183; NID:g180442; PIDN:AAA53287.1; PID:g180444
A;Note: clone CG-beta-a
R;Policastro, P.F.; Daniels-McQueen, S.; Carle, G.; Boime, I.
J. Biol. Chem. 261, 5907-5916, 1986
A;Title: A map of the hCG beta-LH beta gene cluster.
A;Reference number: I55250; MUID:86195987; PMID:2422163
A;Accession: I55250
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5 <PO3>
A;Cross-references: GB:M13504; NID:g180419; PIDN:AAA52005.1; PID:g463088
A;Note: CG-beta-3 gene
A;Accession: I70007
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5 <PO4>
A;Cross-references: GB:M13505; NID:g180429; PIDN:AAA52008.1; PID:g463089
A;Note: CG-beta-6 gene
A;Accession: I70008
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5 <RE5>
A;Cross-references: GB:M13503; NID:g180432; PIDN:AAA52009.1; PID:g463090

A;Note: CG-beta-7 gene
R;Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.
J. Biol. Chem. 256, 1816-1823, 1981
A;Title: The amino acid sequences of the prepeptides contained in the alpha and beta sub
A;Reference number: A92303; MUID:81117268; PMID:7462224
A;Accession: A92303
A;Molecule type: protein
A;Residues: 1-20 <BIR>
A;Note: the identity of the residue at position 19 could not be determined
R;Morgan, F.J.; Birken, S.; Canfield, R.E.
J. Biol. Chem. 250, 5247-5258, 1975
A;Title: The amino acid sequence of human chorionic gonadotropin. The alpha subunit and
A;Reference number: A92181; MUID:75211304; PMID:1150658
A;Accession: A92181
A;Molecule type: protein
A;Residues: 21-165 <MOR>
R;Carlsen, R.B.; Bahl, O.P.; Swaminathan, N.
J. Biol. Chem. 248, 6810-6827, 1973
A;Reference number: A92142; MUID:74011267; PMID:4795659
A;Accession: A92142
A;Molecule type: protein
A;Residues: 21-22,'Q',24-73,'ZL',76-140,142-157,'PB',160-165,'SLP' <CAR>
R;Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.; Wang, Y.
Chinese Biochem. J. 6, 558-562, 1990
A;Title: The immunological characteristics of the enzymatic fragments of human chorionic
A;Reference number: PC1016
A;Accession: PC1016
A;Molecule type: protein
A;Residues: 21-165 <SHI>
A;Note: article in Chinese with English abstract
R;Birken, S.; Armstrong, E.G.; Kolks, M.A.G.; Cole, L.A.; Agosto, G.M.; Krichevsky, A.;
Endocrinology 123, 572-583, 1988
A;Title: Structure of the human chorionic gonadotropin beta-subunit fragment from pregna
A;Reference number: A61097; MUID:88254680; PMID:2454811
A;Accession: A61097
A;Molecule type: protein
A;Residues: 26-32,'X',34-49,'X',51-60;75-112 <BI2>
A;Note: this material from pregancy urine lacks sialic acid in its carbohydrate and has
R;Kardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.
Br. J. Cancer 67, 686-692, 1993
A;Title: Characterisation of UGP and its relationship with beta-core fragment.
A;Reference number: A56873; MUID:93229246; PMID:8471426
A;Accession: B56873
A;Molecule type: protein
A;Residues: 26-28,'X',30-32,'X',34-42,'X',44-45,'X',47-48;75-76,'X',78-91,'G',93-102 <KA
A;Experimental source: urine
A;Note: sequence modified after extraction from NCBI backbone
A;Note: this material was designated urinary gonadotrophin peptide (peak 2)
R;Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader, J.W.; Canfield, R.E.; Machin,
Nature 369, 455-461, 1994
A;Title: Crystal structure of human chorionic gonadotropin.
A;Reference number: A44674; MUID:94261179; PMID:8202136
A;Contents: annotation; X-ray crystallography, 3.0 angstroms; correction of disulfide bo
R;Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
Nature 307, 37-40, 1984
A;Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin an
A;Reference number: I37231; MUID:84093590; PMID:6690982
A;Accession: I37412
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 21-165 <RES>
A;Cross-references: EMBL:X00265; NID:g31719; PIDN:CAA25068.1; PID:g1335075
C;Genetics:
A;Gene: GDB:CGB
A;Cross-references: GDB:119055; OMIM:118860
A;Map position: 19q13.3-19q13.3
A;Introns: 5/3; 61/3
A;Note: the choriogonadotropin beta chain locus contains six genes (or pseudogenes)
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: glycoprotein; hormone; pituitary
F;1-20/Domain: signal sequence #status experimental <SIG>
F;21-165/Product: choriogonadotropin beta chain #status experimental <MAT>
F;29-77,43-92,46-130,54-108,58-110,113-120/Disulfide bonds: #status experimental
F;33,50/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;138,150/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;141,147,152,158/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 58.9%; Score 793; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 5.9e-56;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
Db 22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy 161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
Db 82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy 221 KAPPPSLPSPSRLPGPSDTPILPQ 244
Db 142 KAPPPSLPSPSRLPGPSDTPILPQ 165

RESULT 2
I37231
beta-gonadotropin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jul-2000
C;Accession: I37231
R;Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
Nature 307, 37-40, 1984
A;Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin
A;Reference number: I37231; MUID:84093590; PMID:6690982
A;Accession: I37231
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-145 <RES>
A;Cross-references: EMBL:X00266; NID:g29907; PIDN:CAA25069.1; PID:g1335012
C;Genetics:
A;Introns: 41/3
C;Superfamily: pituitary glycoprotein hormone beta chain

Query Match 58.3%; Score 785; DB 2; Length 145;
Best Local Similarity 99.3%; Pred. No. 2.2e-55;
Matches 143; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
Db 2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy 161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
Db 62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQASSSS 121

Qy 221 KAPPPSLPSPSRLPGPSDTPILPQ 244
Db 122 KAPPPSLPSPSRLPGPSDTPILPQ 145

RESULT 3
KTBAB
choriogonadotropin beta chain precursor - olive baboon
C;Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 28-May-1999
C;Accession: A25808
R;Crawford, R.J.; Tregear, G.W.; Niall, H.D.
Gene 46, 161-169, 1986
A;Title: The nucleotide sequences of baboon chorionic gonadotropin beta-subunit genes
A;Reference number: A25808; MUID:87106851; PMID:2433190
A;Accession: A25808
A;Molecule type: mRNA
A;Residues: 1-165 <CRA>
A;Cross-references: GB:M14966; NID:g176572; PIDN:AAA35383.1; PID:g176573
C;Comment: There are at least five copies of CG-related genes and at least two of the
C;Superfamily: pituitary glycoprotein hormone beta chain

C;Keywords: glycoprotein; hormone; placenta; pregnancy maintenance
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-165/Product: choriogonadotropin beta chain #status predicted <CGB>
F;29-77,43-92,46-130,54-108,58-110,113-120/Disulfide bonds: #status predicted
F;33,50/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;140,147,152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 48.3%; Score 651; DB 1; Length 165;
Best Local Similarity 79.2%; Pred. No. 1.1e-44;
Matches 118; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

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Qy      96 GCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVV 155
           | :  :||||| |||||||||| ||| ||||:||||||||||||| |||| ||| :||||
Db      17 GAQASREPLRPLCRPINATLAAEKEACPVCVTVNTTICAGYCPTMMRVLQAVLPPVPQVV 76

Qy     156 CNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQ 215
           ||||:|||||||||||| ||:|:||  |||||:||||||||:||||||||||||||  |
Db      77 CNYREVRFESIRLPGCPPGVDPMVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPNLQ 136

Qy     216 DSSSSKAPPPSLPSPSRLPGPSDTPILPQ 244
           ||||| |||| |||||| |: || |||
Db     137 ASSSSKDPPPSPPSPSRLLEPAGTPFLPQ 165
```

RESULT 4
UTHUB
lutropin beta chain precursor [validated] - human
N;Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
C;Species: Homo sapiens (man)
C;Date: 13-Jul-1981 #sequence_revision 24-Nov-1999 #text_change 20-Apr-2001
C;Accession: I37994; I58013; A90604; A92759; A94466; A01497; B94552
R;Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
Nature 307, 37-40, 1984
A;Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin an
A;Reference number: I37231; MUID:84093590; PMID:6690982
A;Accession: I37994
A;Status: preliminary; translated from GB/EMBL/DDBJ; not compared with conceptual transl
A;Molecule type: DNA
A;Residues: 1-141 <TAL>
A;Cross-references: GB:X00264; NID:g34351; PIDN:CAA25067.1; PID:g2292893
R;Weiss, J.; Axelrod, L.; Whitcomb, R.W.; Harris, P.E.; Crowley, W.F.; Jameson, J.L.
N. Engl. J. Med. 326, 179-183, 1992
A;Title: Hypogonadism caused by a single amino acid substitution in the beta subunit of
A;Reference number: I58013; MUID:92085985; PMID:1727547
A;Accession: I58013
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 72-73,'R',75-76 <WEI>
A;Cross-references: GB:S71273; NID:g240572; PIDN:AAD14960.1; PID:g4262812
A;Note: mutant sequence from patient with hypogonadism
R;Sairam, M.R.; Li, C.H.
Biochim. Biophys. Acta 412, 70-81, 1975
A;Title: Human pituitary lutropin. Isolation, properties, and the complete amino acid se
A;Reference number: A90604; MUID:76062547; PMID:1191677
A;Accession: A90604
A;Molecule type: protein
A;Residues: 21-38,'Q',40-75,77-131,133-134,'H',136-137 <SAI>
R;Shome, B.; Parlow, A.F.
J. Clin. Endocrinol. Metab. 36, 618-621, 1973
A;Title: The primary structure of the hormone-specific, beta subunit of human pituitary
A;Reference number: A92759; MUID:73090987; PMID:4685398
A;Accession: A92759
A;Molecule type: protein
A;Residues: 21-38,'Q',40-75,77-131,133-134,'H',136-137 <SHO>
R;Closset, J.; Hennen, G.; Lequin, R.M.
FEBS Lett. 29, 97-100, 1973
A;Title: Human luteinizing hormone the amino acid sequence of the beta subunit.
A;Reference number: A91389; MUID:73221227; PMID:4719207
A;Contents: annotation; partial sequence
R;Ward, D.N.
unpublished results, cited by Closset, J., Hennen, G., and Lequin, R.M., FEBS Lett. 29,
A;Reference number: A94466
A;Accession: A94466
A;Molecule type: protein
A;Residues: 21-38,'Q',40-46 <WAR>
A;Note: 28-Val, 33-Arg, and 35-Thr were also found
R;Shome, B.; Parlow, A.F.
submitted to the Atlas, April 1975
A;Reference number: A94552
A;Contents: annotation; binding site
C;Genetics:
A;Gene: GDB:LHB
A;Cross-references: GDB:119364; OMIM:152780
A;Map position: 19q13.3-19q13.3
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: blocked amino end; glycoprotein; hormone; pituitary
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-141/Product: lutropin beta #status experimental <LTB>
F;21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #s
F;29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F;50/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 40.1%; Score 540; DB 1; Length 141;
Best Local Similarity 85.0%; Pred. No. 6.1e-36;
Matches 96; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

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Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
           :||||| | |||| |||||||||||||||||||||||| |||| ||| |||||| |||
Db      22 REPLRPWCHPINAILAVEKEGCPVCITVNTTICAGYCPTMMRVLQAVLPPLPQVVCTYRD 81

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPR 213
           |||||||||||||||:|||| |||||:|  |||||:|||||||||||||| |:
Db      82 VRFESIRLPGCPRGVDPVVSFPVALSCRCGPCRRSTSDCGGPKDHPLTCDHPQ 134
```

RESULT 5
KTHOB
choriogonadotropin beta chain precursor - horse
N;Alternate names: chorionic gonadotropin beta chain (CG); luteinizing hormone (LH) b
C;Species: Equus caballus (domestic horse)
C;Date: 14-Nov-1983 #sequence_revision 03-May-1996 #text_change 18-Jun-1999
C;Accession: A41917; A29304; A29305; A01503
R;Sherman, G.B.; Wolfe, M.W.; Farmerie, T.A.; Clay, C.M.; Threadgill, D.S.; Sharp, D.
Mol. Endocrinol. 6, 951-959, 1992
A;Title: A single gene encodes the beta-subunits of equine luteinizing hormone and ch
A;Reference number: A41917; MUID:92357035; PMID:1379674
A;Accession: A41917
A;Molecule type: DNA
A;Residues: 1-169 <SHE>
A;Cross-references: GB:S41704; NID:g252740; PIDN:AAB22775.1; PID:g252741
A;Experimental source: sperm
A;Note: sequence extracted from NCBI backbone (NCBIN:110184, NCBIP:110185)
R;Sugino, H.; Bousfield, G.R.; Moore Jr., W.T.; Ward, D.N.
J. Biol. Chem. 262, 8603-8609, 1987
A;Title: Structural studies on equine glycoprotein hormones. Amino acid sequence of e
A;Reference number: A29304; MUID:87250475; PMID:3298238
A;Accession: A29304
A;Molecule type: protein
A;Residues: 21-169 <SUG>
R;Bousfield, G.R.; Liu, W.K.; Sugino, H.; Ward, D.N.
J. Biol. Chem. 262, 8610-8620, 1987
A;Title: Structural studies on equine glycoprotein hormones. Amino acid sequence of e
A;Reference number: A29305; MUID:87250476; PMID:3298239
A;Accession: A29305
A;Molecule type: protein
A;Residues: 21-169 <BOU>
R;Ward, D.N.; Moore Jr., W.T.; Burleigh, B.D.
J. Protein Chem. 1, 263-280, 1982
A;Title: Structural studies on equine chorionic gonadotropin.
A;Reference number: A01503
A;Accession: A01503
A;Molecule type: protein
A;Residues: 21-40,'Q',42-43,'SK',46,'XXXX',51,'T',53-64,'T',66-96,'B',98,'R',100-102,
R;Matsui, T.; Mizuochi, T.; Titani, K.; Okinaga, T.; Hoshi, M.; Bousfield, G.R.; Sugi
Biochemistry 33, 14039-14048, 1994
A;Title: Structural analysis of N-linked oligosaccharides of equine chorionic gonadot

```
A;Reference number: A55952; MUID:95034847; PMID:7524670
A;Contents: annotation; glycosylation
A;Note: horse lutropin and choriogonadotropin beta chains have identical protein chains
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: glycoprotein; hormone; pituitary
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-169/Product: choriogonadotropin beta chain #status experimental <MAT>
F;29-77,43-92,46-130,54-108,58-110,113-120/Disulfide bonds: #status predicted
F;33/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             33.0%;  Score 444;  DB 1;  Length 169;
  Best Local Similarity   57.7%;  Pred. No. 3.1e-28;
  Matches   86;  Conservative   16;  Mismatches   39;  Indels    8;  Gaps    2;

Qy    103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
          |||| |||||||||| ||| ||:|||  |:||||||:| ||:   |||:|| || ||::|
Db     24 PLRPLCRPINATLAAEKEACPICITFTTSICAGYCPSMVRVMPAALPAIPQPVCTYRELR 83

Qy    163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKA 222
          | |||||||| ||:|:||: ||||| |  |:  |||||  :| || |     | |||||
Db     84 FASIRLPGCPPGVDPMVSFPVALSCHCGPCQIKTTDCGVFRDQPLACAP---QASSSSKD 140

Qy    223 PPPSLPSPSRLPGP-----SDTPILPQTS 246
          ||    : :  | |     |  |:  :||
Db    141 PPSQPLTSTSTPTPGASRRSSHPLPIKTS 169


RESULT 6
UTBOB
lutropin beta chain precursor - bovine
N;Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 24-Nov-1999
C;Accession: A92534; A92518; A91212; A01499
R;Virgin, J.B.; Silver, B.J.; Thomason, A.R.; Nilson, J.H.
J. Biol. Chem. 260, 7072-7077, 1985
A;Title: The gene for the beta subunit of bovine luteinizing hormone encodes a gonadotro
A;Reference number: A92534; MUID:85207729; PMID:2987241
A;Accession: A92534
A;Molecule type: DNA
A;Residues: 1-141 <VIR>
A;Cross-references: GB:M11506; NID:g163298; PIDN:AAB59267.1; PID:g163299
R;Maurer, R.A.
J. Biol. Chem. 260, 4684-4687, 1985
A;Title: Analysis of several bovine lutropin beta subunit cDNAs reveals heterogeneity in
A;Reference number: A92518; MUID:85182575; PMID:3838746
A;Accession: A92518
A;Molecule type: mRNA
A;Residues: 3-111,'S',113-141 <MAU>
A;Cross-references: GB:M10077; NID:g163300; PIDN:AAA30623.1; PID:g163301
R;Maghuin-Rogister, G.; Hennen, G.
Eur. J. Biochem. 39, 235-253, 1973
A;Title: Luteinizing hormone. The primary structures of the beta-subunit from bovine and
A;Reference number: A91212; MUID:74075724; PMID:4770795
A;Accession: A91212
A;Molecule type: protein
A;Residues: 21-73,'E',75-121,'PG',124-125,'E',127-139 <MAG>
A;Note: some carboxyl-terminal heterogeneity was found
C;Genetics:
A;Introns: 5/3; 61/3
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: blocked amino end; glycoprotein; hormone; pituitary
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-141/Product: lutropin beta #status experimental <LTB>
F;21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #stat
F;29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F;33/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             32.3%;  Score 435;  DB 1;  Length 141;
  Best Local Similarity   65.8%;  Pred. No. 1.3e-27;
  Matches   75;  Conservative   13;  Mismatches   26;  Indels    0;  Gaps    0;

Qy    103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
          |||| |:|||||||| ||| ||||||  |:||||||:| |||  :|| :|| || | ::|
Db     24 PLRPLCQPINATLAAEKEACPVCITFTTSICAGYCPSMKRVLPVILPPMPQRVCTYHELR 83

Qy    163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQD 216
          | |:|||||| ||:|:||: ||||| |  || |:|||||:  || || |   |
Db     84 FASVRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDHPPLPD 137


RESULT 7
UTSHB
lutropin beta chain precursor - sheep
N;Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteini
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 24-Apr-1984 #sequence_revision 19-Jan-2001 #text_change 19-Jan-2001
C;Accession: I46949; S09232; A92110; A90053; B61098; A01500
R;Brown, P.; McNeilly, J.R.; Wallace, R.M.; McNeilly, A.S.; Clark, A.J.
Mol. Cell. Endocrinol. 93, 157-165, 1993
A;Title: Characterization of the ovine LH beta-subunit gene: the promoter directs go
A;Reference number: I46949; MUID:93351742; PMID:8349025
A;Accession: I46949
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-141 <BRO>
A;Cross-references: GB:S64695; NID:g408240; PIDN:AAB27819.1; PID:g408241
R;d'Angelo-Bernard, G.; Moumni, M.; Jutisz, M.; Counis, R.
Nucleic Acids Res. 18, 2175, 1990
A;Title: Cloning and sequence analysis of the cDNA for the precursor of the beta subu
A;Reference number: S09232; MUID:90245669; PMID:2336396
A;Accession: S09232
A;Molecule type: mRNA
A;Residues: 1-58,'L',60-62,'Q',64-141 <ANG>
A;Cross-references: EMBL:X52488; NID:g1319; PIDN:CAA36729.1; PID:g1320
R;Liu, W.K.; Nahm, H.S.; Sweeney, C.M.; Holcomb, G.N.; Ward, D.N.
J. Biol. Chem. 247, 4365-4381, 1972
A;Title: The primary structure of ovine luteinizing hormone. II. The amino acid seque
A;Reference number: A92110; MUID:72211145; PMID:4556309
A;Accession: A92110
A;Molecule type: protein
A;Residues: 21-121,'PG',124-125,'E',127-139 <LIU>
R;Sairam, M.R.; Samy, T.S.A.; Papkoff, H.; Li, C.H.
Arch. Biochem. Biophys. 153, 572-586, 1972
A;Title: The primary structure of ovine interstitial cell-stimulating hormone. II. Th
A;Reference number: A90053; MUID:73190035; PMID:4575435
A;Accession: A90053
A;Molecule type: protein
A;Residues: 21-29,'E',31-71,'P',72-80,'Q',82-121,'PG',124-125,'E',127-139 <SAI>
R;Nomura, K.; Tsunasawa, S.; Ohmura, K.; Sakiyama, F.; Shizume, K.
Endocrinology 123, 700-712, 1988
A;Title: Renotropic activity in ovine luteinizing hormone isoform(s).
A;Reference number: A61098; MUID:88283534; PMID:2456202
A;Accession: B61098
A;Molecule type: protein
A;Residues: 21-39,'N',41-49;64-78,'V',80-82;84-106;115-121,'PG',124-138 <NOM>
A;Note: this form was designated form beta-3; forms beta-1 and beta-2 each lack sever
C;Genetics:
A;Introns: 5/3; 61/3
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: blocked amino end; glycoprotein; hormone; pituitary
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-141/Product: lutropin beta chain #status experimental <MAT>
F;21/Modified site: blocked amino end (Ser) (in mature form) (partial) (probably acet
F;29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F;33/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             32.3%;  Score 435;  DB 1;  Length 141;
  Best Local Similarity   65.8%;  Pred. No. 1.3e-27;
  Matches   75;  Conservative   13;  Mismatches   26;  Indels    0;  Gaps    0;

Qy    103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
          |||| |:|||||||| ||| ||||||  |:||||||:| |||  :|| :|| || | ::|
Db     24 PLRPLCQPINATLAAEKEACPVCITFTTSICAGYCPSMKRVLPVILPPMPQRVCTYHELR 83

Qy    163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQD 216
```

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          | |:|||||| ||:|:||: ||||| |  || |:||||||:  || || |   |
Db     84 FASVRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDHPPLPD 137


RESULT 8
UTRTB
lutropin beta chain precursor - rat
N;Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 24-Sep-1999
C;Accession: A01498; PQ0091; S42527; I83049
R;Jameson, L.; Chin, W.W.; Hollenberg, A.N.; Chang, A.S.; Habener, J.F.
J. Biol. Chem. 259, 15474-15480, 1984
A;Title: The gene encoding the beta-subunit of rat lutenizing hormone. Analysis of gene
A;Reference number: A01498; MUID:85080043; PMID:6096374
A;Accession: A01498
A;Molecule type: DNA
A;Residues: 1-141 <JAM>
A;Cross-references: EMBL:J00749; NID:g205175; PIDN:AAA96703.1; PID:g205176
R;Kato, Y.; Ezashi, T.; Hirai, T.; Kato, T.
submitted to JIPID, July 1990
A;Reference number: PQ0091
A;Accession: PQ0091
A;Molecule type: mRNA
A;Residues: 4-141 <KAT>
R;Chin, W.W.; Godine, J.E.; Klein, D.R.; Chang, A.S.; Tan, L.K.; Habener, J.F.
Proc. Natl. Acad. Sci. U.S.A. 80, 4649-4653, 1983
A;Title: Nucleotide sequence of the cDNA encoding the precursor of the beta subunit of r
A;Reference number: S42527; MUID:83273673; PMID:6192440
A;Accession: S42527
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-141 <CHI>
A;Cross-references: GB:J00749; GB:M54957; NID:g205175; PIDN:AAA96703.1; PID:g205176
R;Kato, Y.; Ezashi, T.; Hirai, T.; Kato, T.
Zool. Sci. 7, 879-887, 1990
A;Title: Strain Difference in Nucleotide Sequences of Rat Glycoprotein Hormone Subunit c
A;Reference number: I60104
A;Accession: I83049
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 4-141 <RES>
A;Cross-references: GB:D00576; NID:g220807; PIDN:BAA00454.1; PID:g220808
C;Comment: The beta chain confers the specificity of the hormone.
C;Genetics:
A;Introns: 5/3; 61/3
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: glycoprotein; hormone; pituitary
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-141/Product: lutropin beta #status predicted <LTB>
F;29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F;33/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            32.1%;  Score 432;  DB 1;  Length 141;
  Best Local Similarity  66.4%;  Pred. No. 2.3e-27;
  Matches   73;  Conservative   15;  Mismatches   22;  Indels    0;  Gaps    0;

Qy    103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
          |||| |||:||||| | | |||||| |:|||||||:| |||   || :|| || ||::|
Db     24 PLRPLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELR 83

Qy    163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 212
          | |:|||||| ||:|:||: |||||:|  || |::|||||:  |:||| |
Db     84 FASVRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMTCDLP 133


RESULT 9
I52320
testicular luteinizing hormone beta-subunit - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C;Accession: I52320
R;Zhang, F.P.; Rannikko, A.; Huhtaniemi, I.
Biochem. Biophys. Res. Commun. 210, 858-865, 1995
A;Title: Isolation and characterization of testis-specific cDNAs for luteinizing horm
A;Reference number: I52320; MUID:95283549; PMID:7763258
A;Accession: I52320
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-139 <RES>
A;Cross-references: EMBL:U25653; NID:g915216; PIDN:AAC52249.1; PID:g915217
C;Genetics:
A;Gene: TLHB1
C;Superfamily: pituitary glycoprotein hormone beta chain

  Query Match            32.0%;  Score 431;  DB 2;  Length 139;
  Best Local Similarity  65.5%;  Pred. No. 2.7e-27;
  Matches   72;  Conservative   16;  Mismatches   22;  Indels    0;  Gaps    0;

Qy    103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
          |||| |||:||||| | | |||||| |:|||||||:| |:|   || :|| || ||::|
Db     22 PLRPLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRILPAALPPVPQPVCTYRELR 81

Qy    163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 212
          | |:|||||| ||:|:||: |||||:|  || |::|||||:  |:||| |
Db     82 FASVRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMTCDLP 131


RESULT 10
JFBY1
mating pheromone alpha-1 precursor - yeast (Saccharomyces cerevisiae)
N;Alternate names: mating factor alpha; mating hormone alpha-1; protein P2209; protei
C;Species: Saccharomyces cerevisiae
C;Date: 24-Apr-1984 #sequence_revision 26-Jul-1996 #text_change 16-Jun-2000
C;Accession: S65199; S65206; A01413; S05790; A91241; A91943
R;Benes, V.; Rechmann, S.; Nentwich, U.; Voss, H.; Ansorge, W.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S65183
A;Accession: S65199
A;Molecule type: DNA
A;Residues: 1-165 <BEN>
A;Cross-references: EMBL:Z73543; NID:g1370390; PIDN:CAA97899.1; PID:g1370391; GSPDB:G
A;Experimental source: strain S288C (AB972)
R;Rieger, M.; Mueller-Auer, S.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S65202
A;Accession: S65206
A;Molecule type: DNA
A;Residues: 1-165 <RIE>
A;Cross-references: EMBL:Z73543; NID:g1370390; PIDN:CAA97899.1; PID:g1370391; GSPDB:G
A;Experimental source: strain S288C (AB972)
R;Kurjan, J.; Herskowitz, I.
Cell 30, 933-943, 1982
A;Title: Structure of a yeast pheromone gene (MFalpha): a putative alpha-factor precu
A;Reference number: A90827; MUID:83050979; PMID:6754095
A;Accession: A01413
A;Molecule type: DNA
A;Residues: 1-41,'S',43-165 <KUR>
A;Cross-references: EMBL:J01340; NID:g171941; PIDN:AAA88727.1; PID:g1197054
A;Experimental source: strain AB320
R;Singh, A.; Chen, E.Y.; Lugovoy, J.M.; Chang, C.N.; Hitzeman, R.A.; Seeburg, P.H.
Nucleic Acids Res. 11, 4049-4063, 1983
A;Title: Saccharomyces cerevisiae contains two discrete genes coding for the alpha-fa
A;Reference number: S05790; MUID:83246532; PMID:6306574
A;Accession: S05790
A;Molecule type: DNA
A;Residues: 1-165 <SIN>
A;Cross-references: EMBL:X01581; NID:g3938; PIDN:CAA25734.1; PID:g3939
R;Stoetzler, D.; Kiltz, H.H.; Duntze, W.
Eur. J. Biochem. 69, 397-400, 1976
A;Title: Primary structure of alpha-factor peptides from Saccharomyces cerevisiae.
A;Reference number: A91241
A;Accession: A91241
A;Molecule type: protein
A;Residues: 90-102 <STO>
A;Experimental source: strain X2180-1B
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R;Tanaka, T.; Kita, H.; Murakami, T.; Narita, K.
J. Biochem. 82, 1681-1687, 1977
A;Title: Purification and amino acid sequence of mating factor from Saccharomyces cerevi
A;Reference number: A91943; MUID:78087498; PMID:340452
A;Accession: A91943
A;Molecule type: protein
A;Residues: 90-102 <TAN>
A;Experimental source: strain X2180-1B
C;Genetics:
A;Gene: SGD:MF(ALPHA)1; MFA1; MIPS:YPL187W
A;Cross-references: SGD:S0006108; MIPS:YPL187w
A;Map position: 16L
C;Function:
A;Description: mediates the conjugation process between the two mating types by inhibiti
C;Superfamily: mating hormone alpha precursor
C;Keywords: duplication; extracellular protein; glycoprotein; hormone; tandem repeat
F;1-19/Domain: signal sequence #status predicted <SIG>
F;84-102,103-123,124-144,145-165/Region: 21-residue repeats
F;90-102/Product: mating pheromone alpha #status experimental <MAT1>
F;111-123/Product: mating pheromone alpha #status experimental <MAT2>
F;132-144/Product: mating pheromone alpha #status experimental <MAT3>
F;153-165/Product: mating pheromone alpha #status experimental <MAT4>
F;23,57,67/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             31.9%;  Score 429.5;  DB 1;  Length 165;
  Best Local Similarity   83.5%;  Pred. No. 4.3e-27;
  Matches   91;  Conservative    6;  Mismatches    5;  Indels    7;  Gaps    2;

Qy       1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSNSTN 60
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYLDLEGDFDVAVLPFSNSTN 60

Qy      61 NGLLFINTTIASIAAKEEGVSLEKREAEA--YVEFDPGCRDLKEPLRPR 107
          |||||||||||||||||||||:|||||  :::  ||     :|:  |
Db      61 NGLLFINTTIASIAAKEEGVSLDKREAEAWHWLQLKPG-----QPMYKR 104


RESULT 11
A61465
lutropin beta chain - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 08-Dec-1995
C;Accession: A61465
R;Glenn, S.D.; Nahm, H.S.; Ward, D.N.
J. Protein Chem. 3, 259-273, 1984
A;Title: The amino acid sequence of the rabbit lutropin beta subunit.
A;Reference number: A61465
A;Accession: A61465
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-119 <GLE>
A;Note: the sequence from Fig. 1 is inconsistent with that from the abstract in having 1
C;Superfamily: pituitary glycoprotein hormone beta chain
F;11-36,25-59,28-90,40-112,74-102,92-95/Disulfide bonds: #status predicted

  Query Match             31.7%;  Score 427;  DB 2;  Length 119;
  Best Local Similarity   67.3%;  Pred. No. 4.8e-27;
  Matches   74;  Conservative   12;  Mismatches   24;  Indels    0;  Gaps    0;

Qy     103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
           |||| |||:|||||  | | ||||||  |:||||||||:| |||    || :|| || ||::|
Db       6 PLRPLCRPVNATLAAENEACPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELR 65

Qy     163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 212
           | |||||||| ||:| ||: |||||:|  || |::||||:  || || |
Db      66 FASIRLPGCPPGVDPEVSFPVALSCRCGPCRLSSSDCGGPRAEPLACDLP 115


RESULT 12
UTPGB
lutropin beta chain precursor - pig
N;Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 30-Jun-1993 #text_change 16-Jun-2000
C;Accession: A48170; A30322; A01501; A60584
R;Ezashi, T.; Hirai, T.; Kato, T.; Wakabayashi, K.; Kato, Y.
J. Mol. Endocrinol. 5, 137-146, 1990
A;Title: The gene for the beta subunit of porcine LH: clusters of GC boxes and CACCC
A;Reference number: A48170; MUID:91063934; PMID:1701088
A;Accession: A48170
A;Molecule type: DNA
A;Residues: 1-141 <EZA>
A;Cross-references: GB:D00579; NID:g217693; PIDN:BAA00457.1; PID:g217694
R;Kato, Y.; Hirai, T.
Mol. Cell. Endocrinol. 62, 47-53, 1989
A;Title: Cloning and DNA sequence analysis of the cDNA for the precursor of porcine l
A;Reference number: A30322; MUID:89306142; PMID:2744222
A;Accession: A30322
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-141 <KAT>
R;Maghuin-Rogister, G.; Hennen, G.
Eur. J. Biochem. 39, 235-253, 1973
A;Title: Luteinizing hormone. The primary structures of the beta-subunit from bovine
A;Reference number: A91212; MUID:74075724; PMID:4770795
A;Accession: A01501
A;Molecule type: protein
A;Residues: 21-29,'Z',31-39,'D',41-61,'R',63-82,'I',84-86,'S',88-121,'PG',124-133,'P
A;Note: 30-Arg was also found
A;Note: about half the chains lack one or both carboxyl-terminal leucines
R;Nomura, K.; Ohmura, K.; Nakamura, Y.; Horiba, N.; Shirakura, Y.; Sato, Y.; Ujihara,
Endocrinology 124, 712-719, 1989
A;Title: Porcine luteinizing hormone isoform(s): relationship between their molecular
A;Reference number: A60584; MUID:89107050; PMID:2536317
A;Accession: A60584
A;Molecule type: protein
A;Residues: 21-31;137-139 <NOM>
A;Note: the lutropin beta chain is heterogeneous at the carboxyl end; this form lacke
C;Genetics:
A;Introns: 5/3; 61/3
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: blocked amino end; glycoprotein; hormone
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-141/Product: lutropin beta chain #status experimental <MAT>
F;21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #s
F;29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F;33/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             31.6%;  Score 425;  DB 1;  Length 141;
  Best Local Similarity   67.3%;  Pred. No. 8.3e-27;
  Matches   74;  Conservative   10;  Mismatches   26;  Indels    0;  Gaps    0;

Qy     103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
           |||| |||||||||| | | ||||||  |:||||||||:| |||    || :|| || ||::
Db      24 PLRPLCRPINATLAAENEACPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELS 83

Qy     163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 212
           | |||||||| ||:| ||: ||||| |  || |::||||:  || || |
Db      84 FASIRLPGCPPGVDPTVSFPVALSCHCGPCRLSSSDCGGPRAQPLACDRP 133


RESULT 13
JC4527
luteinizing hormone beta chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 16-Jul-1999
C;Accession: JC4527
R;Kumar, T.R.; Matzuk, M.M.
Gene 166, 335-336, 1995
A;Title: Cloning of the mouse gonadotropin beta-subunit-encoding genes, II. Structure
A;Reference number: JC4527; MUID:96125216; PMID:8543188
A;Accession: JC4527
A;Molecule type: mRNA
A;Residues: 1-141 <KUM>
A;Cross-references: GB:U25145; NID:g930344; PIDN:AAA92841.1; PID:g930345
A;Experimental source: 129SvEv
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C;Comment: This protein is co-produced with follicle-stimulating hormone in pituitary gc
n reproduction including gonadal growth, gametogenesis and steroidogenesis.
C;Genetics:
A;Gene: lh beta
A;Introns: 5/3; 61/3
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: hormone; reproduction
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-141/Product: luteinizing hormone beta chain #status predicted <MAT>

  Query Match             31.3%;  Score 421;  DB 2;  Length 141;
  Best Local Similarity   64.5%;  Pred. No. 1.7e-26;
  Matches   71;  Conservative   15;  Mismatches   24;  Indels    0;  Gaps    0;

Qy    103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
          |||| |||:||||| | | |||||| |:||||||:| |||   || :|| || ||::
Db     24 PLRPLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELA 83

Qy    163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 212
          | |:|||||| ||:|:||: |||||:|  || |::|||||:  |: || |
Db     84 FASVRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMACDLP 133


RESULT 14
S00512
lutropin beta chain precursor - dog (fragment)
N;Alternate names: luteinizing hormone beta chain
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Accession: S00512
R;Wolf, D.L.; Appleby, V.L.; Hjerrild, K.; Baker, A.R.; Talmadge, K.
Nucleic Acids Res. 15, 10602, 1987
A;Title: Nucleic acid and amino acid sequences of dog beta-LH: comparison to rat, cow an
A;Reference number: S00512; MUID:88096605; PMID:3697104
A;Accession: S00512
A;Molecule type: mRNA
A;Residues: 1-138 <WOL>
A;Cross-references: EMBL:Y00518; NID:g907; PIDN:CAA68572.1; PID:g860906
C;Superfamily: pituitary glycoprotein hormone beta chain
F;1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F;18-138/Product: lutropin beta chain #status predicted <MAT>
F;26-51,40-74,43-105,55-127,89-117,107-110/Disulfide bonds: #status predicted

  Query Match             31.0%;  Score 418;  DB 2;  Length 138;
  Best Local Similarity   66.4%;  Pred. No. 2.9e-26;
  Matches   73;  Conservative   10;  Mismatches   27;  Indels    0;  Gaps    0;

Qy    103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
          |||| |||||||||| | | |||||| ||||||||:| |||   || :|| || | ::
Db     21 PLRPLCRPINATLAAENEACPVCITFTTTICAGYCPSMVRVLPAALPPVPQPVCTYHELH 80

Qy    163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 212
          | |||||||| ||:|:||: |||||:|  || | :|||||:   | || |
Db     81 FASIRLPGCPPGVDPMVSFPVALSCRCGPCRLSNSDCGGPRAQSLACDRP 130


RESULT 15
PN0139
lutropin beta chain - minke whale
N;Alternate names: luteinizing hormone beta chain
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 08-Dec-1995
C;Accession: PN0139
R;Karasev, V.S.; Pankov, Y.A.
Biokhimiia 50, 1972-1986, 1985
A;Title: Amino acid sequence of reduced and carboxymethylated alpha- and beta-subunits c
A;Reference number: PN0138
A;Accession: PN0139
A;Molecule type: protein
A;Residues: 1-118 <KAR>
A;Note: article in Russian with English abstract
C;Superfamily: pituitary glycoprotein hormone beta chain
C;Keywords: glycoprotein; hormone
F;9-34,23-57,26-88,38-110,72-100,90-93/Disulfide bonds: #status predicted
F;13/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             30.2%;  Score 407;  DB 2;  Length 118;
  Best Local Similarity   56.0%;  Pred. No. 1.8e-25;
  Matches   70;  Conservative   18;  Mismatches   27;  Indels   10;  Gaps    1;

Qy    103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
          |||| |||||||||| : : ||||||  |:||||||:| |||   || :|: || ||::|
Db      4 PLRPLCRPINATLAAZBZACPVCITFTTSICAGYCPSMVRVLPAALPPVPZPVCTYRZLR 63

Qy    163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKA 222
          | |||||||| ||:|:||: ||||| |  || |:::||  :  || |:          ::
Db     64 FASIRLPGCPPGVBPMVSFPVALSCHCGPCRLSSSBCGPGRAZPLACB----------RS 113

Qy    223 PPPSL 227
          | | |
Db    114 PRPGL 118


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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:26 ; Search time 9.98601 Seconds
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Perfect score: 1347
Sequence: 1 MRFPSIFTAVLFAASSALAA.....LPGPSDTPILPQTSHHHHHH 252

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	793	58.9	165	1	CGHB_HUMAN	P01233 homo sapien
2	651	48.3	165	1	CGHB_PAPAN	P07434 papio anubi
3	540	40.1	141	1	LSHB_HUMAN	P01229 homo sapien
4	516.5	38.3	164	1	CGHB_CALJA	P51500 callithrix
5	474	35.2	169	1	LSHB_EQUBU	O46641 equus burch
6	459	34.1	169	1	LSHB_EQUAS	P19794 equus asinu
7	444	33.0	143	1	LSHB_FELCA	O77805 felis silve
8	444	33.0	169	1	LSHB_HORSE	P08751 equus cabal
9	435	32.3	141	1	LSHB_BOVIN	P04651 bos taurus
10	432	32.1	141	1	LSHB_RAT	P01230 rattus norv
11	429.5	31.9	144	1	MFA1_SACBA	P25501 saccharomyc
12	429.5	31.9	165	1	MFA3_YEAST	P01149 saccharomyc
13	429.5	31.9	186	1	MFAI_YEAST	P25041 saccharomyc
14	426	31.6	141	1	LSHB_CERSI	O77835 ceratotheri
15	425	31.6	141	1	LSHB_PIG	P01232 sus scrofa
16	425	31.6	141	1	LSHB_SHEEP	P01231 ovis aries
17	421	31.3	141	1	LSHB_MOUSE	O09108 mus musculu
18	418	31.0	138	1	LSHB_CANFA	P18842 canis famil
19	407	30.2	118	1	LSHB_BALAC	P33088 balaenopter
20	406	30.1	118	1	LSHB_PHYCA	P25330 physeter ca
21	405	30.1	128	1	LSHB_PHOSU	Q9qya9 phodopus su
22	402	29.8	138	1	LSHB_MACRU	O46483 macropus ru
23	393	29.2	141	1	LSHB_TRIVU	O46482 trichosurus
24	303	22.5	140	1	GTH2_CARAU	Q98849 carassius a
25	303	22.5	144	1	GTH2_CYPCA	P01235 cyprinus ca
26	301	22.3	141	1	GTH2_HYPMO	P37038 hypophthalm
27	301	22.3	146	1	GTH2_CTEID	P30984 ctenopharyn
28	291	21.6	142	1	GTH2_ONCKE	P10256 oncorhynchu
29	288	21.4	142	1	GTH2_ONCMA	P48253 oncorhynchu
30	284	21.1	140	1	GTH2_ICTPU	Q9dg80 ictalurus p
31	283	21.0	138	1	GTH2_CLAGA	P53543 clarias gar
32	282	20.9	149	1	GTH2_CLUPA	Q9ygh2 clupea pall
33	278	20.6	142	1	GTH2_ONCTS	P07732 oncorhynchu
34	276.5	20.5	113	1	GTHB_MURCI	P12837 muraenesox
35	273	20.3	140	1	GTH2_ANGAN	P27767 anguilla an
36	273	20.3	142	1	GTH2_CORAU	P48251 coregonus a
37	269	20.0	128	1	LSHB_STRCA	P80664 struthio ca
38	265	19.7	112	1	LSHB_RANCA	P80071 rana catesb
39	260	19.3	159	1	LSHB_MELGA	P45646 meleagris g
40	258	19.2	166	1	LSHB_COTJA	P45657 coturnix co
41	257	19.1	137	1	GTH2_ACALA	Q90225 acanthopagr
42	255	18.9	139	1	GTH2_MORSA	Q91121 morone saxa
43	255	18.9	146	1	GTH2_TRITC	Q9pw98 trichogaste
44	254	18.9	138	1	TSHB_CANFA	P54828 canis famil
45	253	18.8	127	1	GTH1_ANGJA	Q9ygk3 anguilla ja

ALIGNMENTS

RESULT 1
CGHB_HUMAN
ID CGHB_HUMAN STANDARD; PRT; 165 AA.
AC P01233; Q14000; Q13991;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Choriogonadotropin beta chain precursor (Chorionic gonadotrophin beta
DE subunit) (CG-beta).
GN CGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012134; PubMed=6774259;
RA Fiddes J.C., Goodman H.M.;
RT "The cDNA for the beta-subunit of human chorionic gonadotropin
RT suggests evolution of a gene by readthrough into the 3'-untranslated
RT region.";
RL Nature 286:684-687(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84093590; PubMed=6690982;
RA Talmadge K., Vamvakopoulos N.C., Fiddes J.C.;
RT "Evolution of the genes for the beta subunits of human chorionic
RT gonadotropin and luteinizing hormone.";
RL Nature 307:37-40(1984).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=84008141; PubMed=6194155;
RA Policastro P., Ovitt C.E., Hoshina M., Fukuoka H., Boothby M.R.,
RA Boime I.;
RT "The beta subunit of human chorionic gonadotropin is encoded by
RT multiple genes.";
RL J. Biol. Chem. 258:11492-11499(1983).
RN [4]
RP SEQUENCE OF 1-20.
RX MEDLINE=81117268; PubMed=7462224;
RA Birken S., Fetherston J., Canfield R.E., Boime I.;
RT "The amino acid sequences of the prepeptides contained in the alpha
RT and beta subunits of human choriogonadotropin.";
RL J. Biol. Chem. 256:1816-1823(1981).
RN [5]
RP SEQUENCE OF 21-165.
RX MEDLINE=75211304; PubMed=1150658;
RA Morgan F.J., Birken S., Canfield R.E.;
RT "The amino acid sequence of human chorionic gonadotropin. The alpha
RT subunit and beta subunit.";
RL J. Biol. Chem. 250:5247-5258(1975).
RN [6]
RP PRELIMINARY SEQUENCE OF 21-165.
RX MEDLINE=74011267; PubMed=4795659;
RA Carlsen R.B., Bahl O.P., Swaminathan N.;
RT "Human chorionic gonadotropin. Linear amino acid sequence of the beta

```
RT   subunit.";
RL   J. Biol. Chem. 248:6810-6827(1973).
RN   [7]
RP   SEQUENCE OF 1-5 FROM N.A.
RX   MEDLINE=86195987; PubMed=2422163;
RA   Policastro P.F., Daniels-Mcqueen S., Carle G., Boime I.;
RT   "A map of the hCG beta-LH beta gene cluster.";
RL   J. Biol. Chem. 261:5907-5916(1986).
RN   [8]
RP   PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX   MEDLINE=81215630; PubMed=7240231;
RA   Mise T., Bahl O.P.;
RT   "Assignment of disulfide bonds in the beta subunit of human chorionic
RT   gonadotropin.";
RL   J. Biol. Chem. 256:6587-6592(1981).
RN   [9]
RP   DISULFIDE BONDS.
RX   MEDLINE=90094415; PubMed=1688430;
RA   Saccuzo Beebe J., Mountjoy K., Krzesicki R.F., Perini F.,
RA   Ruddon R.W.;
RT   "Role of disulfide bond formation in the folding of human chorionic
RT   gonadotropin beta subunit into an alpha beta dimer assembly-competent
RT   form.";
RL   J. Biol. Chem. 265:312-317(1990).
RN   [10]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE=92314469; PubMed=1820200;
RA   Weisshaar G., Hiyama J., Renwick A.G.C.;
RT   "Site-specific N-glycosylation of human chorionic gonadotrophin --
RT   structural analysis of glycopeptides by one- and two-dimensional 1H
RT   NMR spectroscopy.";
RL   Glycobiology 1:393-404(1991).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX   MEDLINE=94261179; PubMed=8202136;
RA   Lapthorn A.J., Harris D.C., Littlejohn A., Lustbader J.W.,
RA   Canfield R.E., Machin K.J., Morgan F.J., Isaacs N.W.;
RT   "Crystal structure of human chorionic gonadotropin.";
RL   Nature 369:455-461(1994).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
CC   -!- DEVELOPMENTAL STAGE: MADE BY THE FIRST TRIMESTER PLACENTA.
CC   -!- PHARMACEUTICAL: Available under the names Novarel (Ferring) and
CC       Profasi (Serono).
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00117; AAA96690.1; -.
DR   EMBL; X00265; CAA25068.1; ALT_INIT.
DR   EMBL; X00266; CAA25069.1; ALT_INIT.
DR   EMBL; M13504; AAA52005.1; -.
DR   EMBL; M13505; AAA52008.1; -.
DR   EMBL; M13503; AAA52009.1; -.
DR   EMBL; K03189; AAA53288.1; -.
DR   EMBL; K03187; AAA53288.1; JOINED.
DR   EMBL; K03188; AAA53288.1; JOINED.
DR   EMBL; K03183; AAA53287.1; -.
DR   EMBL; K00092; AAA53287.1; JOINED.
DR   EMBL; K03182; AAA53287.1; JOINED.
DR   PIR; A01502; KTHUB.
DR   PDB; 1HCN; 30-SEP-94.
DR   PDB; 1HRP; 01-NOV-94.
DR   PDB; 1XUL; 15-MAY-97.
DR   GlycoSuiteDB; P01233; -.
DR   Genew; HGNC:1886; CGB.
DR   Genew; HGNC:16451; CGB7.
DR   Genew; HGNC:16452; CGB5.
DR   MIM; 118860; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Glycoprotein; Signal; Pharmaceutical; 3D-structure.
FT   SIGNAL        1     20
FT   CHAIN        21    165       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77
FT   DISULFID     43     92
FT   DISULFID     46    130
FT   DISULFID     54    108
FT   DISULFID     58    110
FT   DISULFID    113    120
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .).
FT                                /FTId=CAR_000042.
FT   CARBOHYD     50     50       N-LINKED (GLCNAC. . .).
FT                                /FTId=CAR_000043.
FT   CARBOHYD    141    141       O-LINKED.
FT   CARBOHYD    147    147       O-LINKED.
FT   CARBOHYD    152    152       O-LINKED.
FT   CARBOHYD    158    158       O-LINKED.
FT   VARIANT     137    137       D -> A (IN GENE 6).
FT                                /FTId=VAR_003188.
FT   CONFLICT     24     24       P -> M (IN REF. 3; AAA53287).
SQ   SEQUENCE   165 AA;  17739 MW;  5598FB9E51A05748 CRC64;

  Query Match             58.9%;  Score 793;  DB 1;  Length 165;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-59;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy     221 KAPPPSLPSPSRLPGPSDTPILPQ 244
           ||||||||||||||||||||||||
Db     142 KAPPPSLPSPSRLPGPSDTPILPQ 165


RESULT 2
CGHB_PAPAN
ID   CGHB_PAPAN     .STANDARD;      PRT;   165 AA.
AC   P07434;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-APR-1988 (Rel. 07, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Choriogonadotropin beta chain precursor (Chorionic gonadotrophin beta
DE   subunit) (CG-beta).
GN   CGB.
OS   Papio anubis (Olive baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Papio.
OX   NCBI_TaxID=9555;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87106851; PubMed=2433190;
RA   Crawford R.J., Tregear G.W., Niall H.D.;
```

```
RT   "The nucleotide sequences of baboon chorionic gonadotropin
RT   beta-subunit genes have diverged from the human.";
RL   Gene 46:161-169(1986).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
CC   -!- MISCELLANEOUS: THERE ARE AT LEAST FIVE COPIES OF CG-RELATED GENES
CC       AND AT LEAST TWO OF THESE ARE EXPRESSED IN THE BABOON PLACENTA.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M14966; AAA35383.1; -.
DR   PIR; A25808; KTBAB.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Glycoprotein; Signal.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   CHAIN        21    165       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD     50     50       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    141    141       O-LINKED (BY SIMILARITY).
FT   CARBOHYD    147    147       O-LINKED (BY SIMILARITY).
FT   CARBOHYD    152    152       O-LINKED (BY SIMILARITY).
SQ   SEQUENCE   165 AA;  17592 MW;  36D3E207A9F1E1C3 CRC64;

  Query Match             48.3%;  Score 651;  DB 1;  Length 165;
  Best Local Similarity   79.2%;  Pred. No. 2.7e-47;
  Matches  118;  Conservative   10;  Mismatches   21;  Indels    0;  Gaps    0;

Qy      96 GCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVV 155
           | :  :||||| |||||||||| ||| ||||:||||||||||||||| |||| ||| :||||
Db      17 GAQASREPLRPLCRPINATLAAEKEACPVCVTVNTTICAGYCPTMMRVLQAVLPPVPQVV 76

Qy     156 CNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQ 215
           ||||:|||||||||||| ||:|:|| |||||:||||||||:|||||||||||||  |
Db      77 CNYREVRFESIRLPGCPPGVDPMVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPNLQ 136

Qy     216 DSSSSKAPPPSLPSPSRLPGPSDTPILPQ 244
            ||||| |||| |||||| |: || |||
Db     137 ASSSSKDPPPSPPSPSRLLEPAGTPFLPQ 165


RESULT 3
LSHB_HUMAN
ID   LSHB_HUMAN     STANDARD;      PRT;   141 AA.
AC   P01229;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE   beta) (LSH-B) (LH-B).
GN   LHB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84093590; PubMed=6690982;
RA   Talmadge K., Vamvakopoulos N.C., Fiddes J.C.;
RT   "Evolution of the genes for the beta subunits of human chorionic
RT   gonadotropin and luteinizing hormone.";
RL   Nature 307:37-40(1984).
RN   [2]
RP   SEQUENCE OF 21-141.
RX   MEDLINE=76062547; PubMed=1191677;
RA   Sairam M.R., Li C.H.;
RT   "Human pituitary lutropin. Isolation, properties, and the complete
RT   amino acid sequence of the beta-subunit.";
RL   Biochim. Biophys. Acta 412:70-81(1975).
RN   [3]
RP   PRELIMINARY SEQUENCE OF 21-141.
RX   MEDLINE=73090987; PubMed=4685398;
RA   Shome B., Parlow A.F.;
RT   "The primary structure of the hormone-specific, beta subunit of human
RT   pituitary luteinizing hormone (hLH).";
RL   J. Clin. Endocrinol. Metab. 36:618-621(1973).
RN   [4]
RP   PRELIMINARY PARTIAL SEQUENCE.
RX   MEDLINE=73221227; PubMed=4719207;
RA   Closset J., Hennen G., Lequin R.M.;
RT   "Human luteinizing hormone. The amino acid sequence of the
RT   subunit.";
RL   FEBS Lett. 29:97-100(1973).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATE.
RX   MEDLINE=91122088; PubMed=1991473;
RA   Weisshaar G., Hiyama J., Renwick A.G.C., Nimtz M.;
RT   "NMR investigations of the N-linked oligosaccharides at individual
RT   glycosylation sites of human lutropin.";
RL   Eur. J. Biochem. 195:257-268(1991).
RN   [6]
RP   STRUCTURE BY NMR OF 58-77.
RX   MEDLINE=92357029; PubMed=1495492;
RA   Keutmann H.T., Hua Q.-X., Weiss M.A.;
RT   "Structure of a receptor-binding fragment from human luteinizing
RT   hormone beta-subunit determined by [1H]- and [15N]nuclear magnetic
RT   resonance spectroscopy.";
RL   Mol. Endocrinol. 6:904-913(1992).
RN   [7]
RP   VARIANT ARG-74.
RX   MEDLINE=92085985; PubMed=1727547;
RA   Weiss J., Axelrod L., Whitcomb R.W., Harris P.E., Crowley W.F.,
RA   Jameson J.L.;
RT   "Hypogonadism caused by a single amino acid substitution in the beta
RT   subunit of luteinizing hormone.";
RL   New Engl. J. Med. 326:179-183(1992).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PITUITARY.
CC   -!- DISEASE: DEFECTS IN LHB ARE A CAUSE OF HYPOGONADISM WHICH IS
CC       CHARACTERIZED BY INFERTILITY AND PSEUDOHERMAPHRODITISM.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
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CC   ---------------------------------------------------------------------------
DR   EMBL; X00264; CAA25067.1; -.
DR   EMBL; S71273; AAD14960.1; ALT_SEQ.
DR   PIR; A01497; UTHUB.
DR   HSSP; P01233; 1XUL.
DR   GlycoSuiteDB; P01229; -.
DR   Genew; HGNC:6584; LHB.
DR   MIM; 152780; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Glycoprotein; Signal; Pseudohermaphroditism;
KW   Disease mutation.
FT   SIGNAL       1     20
FT   CHAIN       21    141       LUTROPIN BETA CHAIN.
FT   DISULFID    29     77       BY SIMILARITY.
FT   DISULFID    43     92       BY SIMILARITY.
FT   DISULFID    46    130       BY SIMILARITY.
FT   DISULFID    54    108       BY SIMILARITY.
FT   DISULFID    58    110       BY SIMILARITY.
FT   DISULFID   113    120       BY SIMILARITY.
FT   CARBOHYD    50     50       N-LINKED (GLCNAC. . .).
FT                               /FTId=CAR_000045.
FT   VARIANT     74     74       Q -> R (IN HYPOGONADISM; LACK OF
FT                               RECEPTOR-BINDING).
FT                               /FTId=VAR_003189.
FT   CONFLICT    39     39       E -> Q (IN REF. 2).
FT   CONFLICT    76     76       MISSING (IN REF. 2).
FT   CONFLICT   132    135       HPQL -> PQH (IN REF. 2).
SQ   SEQUENCE   141 AA;  15345 MW;  E411766253113F7C CRC64;

  Query Match             40.1%;  Score 540;  DB 1;  Length 141;
  Best Local Similarity   85.0%;  Pred. No. 3.7e-38;
  Matches   96;  Conservative    6;  Mismatches   11;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
          :||||| | |||| ||||||||||||||||||||||||| |||| ||| |||||| |||
Db     22 REPLRPWCHPINAILAVEKEGCPVCITVNTTICAGYCPTMMRVLQAVLPPLPQVVCTYRD 81

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPR 213
          |||||||||||||||:|||| ||||||:|  |||||:||||||||||||| |:
Db     82 VRFESIRLPGCPRGVDPVVSFPVALSCRCGPCRRSTSDCGGPKDHPLTCDHPQ 134


RESULT 4
CGHB_CALJA
ID   CGHB_CALJA     STANDARD;      PRT;   164 AA.
AC   P51500;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Choriogonadotropin beta chain precursor (Chorionic gonadotrophin beta
DE   subunit) (CG-beta).
GN   CGB.
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC   Callithrix.
OX   NCBI_TaxID=9483;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=96115012; PubMed=7492691;
RA   Simula A.P., Amato F., Faast R., Lopata A., Berka J., Norman R.J.;
RT   "Luteinizing hormone/chorionic gonadotropin bioactivity in the common
RT   marmoset (Callithrix jacchus) is due to a chorionic gonadotropin
RT   molecule with a structure intermediate between human chorionic
RT   gonadotropin and human luteinizing hormone.";
RL   Biol. Reprod. 53:380-389(1995).
CC   -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC       ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- TISSUE SPECIFICITY: PLACENTA.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; U04447; AAC00029.1; -.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Glycoprotein; Signal.
FT   SIGNAL       1     20       BY SIMILARITY.
FT   CHAIN       21    164       CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID    29     77       BY SIMILARITY.
FT   DISULFID    43     92       BY SIMILARITY.
FT   DISULFID    46    130       BY SIMILARITY.
FT   DISULFID    54    108       BY SIMILARITY.
FT   DISULFID    58    110       BY SIMILARITY.
FT   DISULFID   113    120       BY SIMILARITY.
FT   CARBOHYD    50     50       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD   146    146       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD   151    151       O-LINKED (BY SIMILARITY).
SQ   SEQUENCE   164 AA;  17712 MW;  0CD92EDDC2618FA6 CRC64;

  Query Match             38.3%;  Score 516.5;  DB 1;  Length 164;
  Best Local Similarity   66.0%;  Pred. No. 3.9e-36;
  Matches   95;  Conservative   17;  Mismatches   31;  Indels    1;  Gaps    1;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
          |||||| |||:|| || |||||||||:  ||||||||| :| |||| :|| ||| |||| :
Db     22 KEPLRPLCRPVNAILAAEKEGCPVCVAFNTTICAGYCSSMVRVLQTILPPLPQSVCNYHE 81

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
          :|| |:|||||  ||:|||| |||||:| |||| :||| :: || ||   ||| |||
Db     82 LRFTSVRLPGCRPGVDPVVSMPVALSCRCGLCRRSYSDCGSLRNEPLGCDYSTFQD-SSS 140

Qy    221 KAPPPSLPSPSRLPGPSDTPILPQ 244
          | || :| |||:|  |:| |::||
Db    141 KDPPRNLTSPSQLLEPADPPLVPQ 164


RESULT 5
LSHB_EQUBU
ID   LSHB_EQUBU     STANDARD;      PRT;   169 AA.
AC   O46641;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Lutropin/choriogonadotropin beta chain precursor (LSH-B/CG-B)
DE   (Lutenizing hormone beta subunit).
GN   LHB.
OS   Equus burchelli (Plains zebra) (Equus quagga).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9790;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pituitary;
RX   MEDLINE=99273280; PubMed=10341734;
RA   Chopineau M., Martinat N., Pourchet C., Stewart F., Combarnous Y.,
RA   Guillou F.;
RT   "Cloning, sequencing and functional expression of zebra (Equus
RT   burchelli) LH.";
RL   J. Reprod. Fertil. 115:159-166(1999).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y16265; CAA76146.1; -.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Glycoprotein; Signal.
FT   SIGNAL       1     20       BY SIMILARITY.
FT   CHAIN       21    169       LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID    29     77       BY SIMILARITY.
FT   DISULFID    43     92       BY SIMILARITY.
FT   DISULFID    46    130       BY SIMILARITY.
FT   DISULFID    54    108       BY SIMILARITY.
FT   DISULFID    58    110       BY SIMILARITY.
FT   DISULFID   113    120       BY SIMILARITY.
FT   CARBOHYD    33     33       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   158    158       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   169 AA;  17824 MW;  322DF724AEAA93E9 CRC64;

  Query Match             35.2%;  Score 474;  DB 1;  Length 169;
  Best Local Similarity   60.5%;  Pred. No. 1.4e-32;
  Matches   89;  Conservative   16;  Mismatches   32;  Indels   10;  Gaps    3;

Qy    103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
          |||| |||||||||| ||| ||:||| |:||||||||:| ||:   || :|| || ||::|
Db     24 PLRPLCRPINATLAAEKEACPICITFTTSICAGYCPSMVRVMPAALPPIPQPVCTYRELR 83

Qy    163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKA 222
          | |||||||| ||:|:||: ||||| |  ||  |||||||:|||| |     | |||||
Db     84 FASIRLPGCPPGVDPMVSFPVALSCHCGPCRLKTTDCGGPRDHPLACAP---QASSSSKD 140

Qy    223 PP--PSLPSPSRLPGPSDTPILPQTSH 247
          ||  |   : :  || |:     ::||
Db    141 PPSQPLTSTSTPTPGASN-----RSSH 162


RESULT 6
LSHB_EQUAS
ID   LSHB_EQUAS     STANDARD;      PRT;   169 AA.
AC   P19794;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Lutropin/choriogonadotropin beta chain precursor (LSH-B/CG-B)
DE   (Lutenizing hormone beta subunit).
GN   LHB.
OS   Equus asinus (Donkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9793;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chopineau M., Combarnous Y., Allen W.R., Stewart F.;
RL   Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   PRELIMINARY SEQUENCE OF 105-169 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=90262634; PubMed=2344391;
RA   Leigh S.E.A., Stewart F.;
RT   "Partial cDNA sequence for the donkey chorionic gonadotrophin-beta
RT   subunit suggests evolution from an ancestral LH-beta gene.";
RL   J. Mol. Endocrinol. 4:143-150(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X80116; CAA56422.1; -.
DR   EMBL; X53669; CAA37709.1; ALT_SEQ.
DR   PIR; S15676; S15676.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Glycoprotein; Signal.
FT   SIGNAL       1     20       BY SIMILARITY.
FT   CHAIN       21    169       LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID    29     77       BY SIMILARITY.
FT   DISULFID    43     92       BY SIMILARITY.
FT   DISULFID    46    130       BY SIMILARITY.
FT   DISULFID    54    108       BY SIMILARITY.
FT   DISULFID    58    110       BY SIMILARITY.
FT   DISULFID   113    120       BY SIMILARITY.
FT   CARBOHYD    33     33       N-LINKED (GLCNAC. . .) (PROBABLE).
SQ   SEQUENCE   169 AA;  17943 MW;  AEED20891E96FA7C CRC64;

  Query Match             34.1%;  Score 459;  DB 1;  Length 169;
  Best Local Similarity   57.9%;  Pred. No. 2.4e-31;
  Matches   84;  Conservative   15;  Mismatches   38;  Indels    8;  Gaps    1;

Qy    103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
          |||| |||||||||| ||| ||:||| |:|||||| :| ||:   || :|| || ||::|
Db     24 PLRPLCRPINATLAAEKEACPICITFTTSICAGYCRSMVRVMPAALPPIPQPVCTYRELR 83

Qy    163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPL--------TCDDPRF 214
          | |||||||| ||:|:||: ||||| |  ||  |||||||:||||        :| ||
Db     84 FGSIRLPGCPPGVDPMVSFPVALSCHCGPCRLKTTDCGGPRDHPLACAPQTSSSCKDPPS 143
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Qy     215 QDSSSSKAPPPSLPSPSRLPGPSDT 239
           |  :|:  | |     |  | | :|
Db     144 QPLTSTSTPTPGASRRSSHPLPINT 168


RESULT 7
LSHB_FELCA
ID   LSHB_FELCA     STANDARD;      PRT;   143 AA.
AC   O77805;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE   beta) (LSH-B) (LH-B).
GN   LHB.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pituitary;
RA   Pukazhenthi B.S., Varma G.M., Brown J.L.;
RT   "Molecular cloning and sequence analysis of the cDNA for the feline
RT   luteinizing hormone beta subunit.";
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF095716; AAC64196.1; -.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    143       LUTROPIN BETA CHAIN.
FT   DISULFID     31     79       BY SIMILARITY.
FT   DISULFID     45     94       BY SIMILARITY.
FT   DISULFID     48    132       BY SIMILARITY.
FT   DISULFID     56    110       BY SIMILARITY.
FT   DISULFID     60    112       BY SIMILARITY.
FT   DISULFID    115    122       BY SIMILARITY.
FT   CARBOHYD     35     35       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   143 AA;  15318 MW;  C5C55DDC907422DB CRC64;

  Query Match             33.0%;  Score 444;  DB 1;  Length 143;
  Best Local Similarity   67.9%;  Pred. No. 3.5e-30;
  Matches   76;  Conservative   13;  Mismatches   23;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
           :|||||  |||||||||| | | ||||:|  ||||||||||:| |||   || :|| || ||:
Db      24 REPLRPLCRPINATLAAENEACPVCVTFTTTICAGYCPSMMRVLPAALPPVPQPVCTYRE 83

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 212
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           :|| |:|||||| ||:||||: |||||:|  || |::|||||:  || || |
Db      84 LRFASVRLPGCPPGVDPVVSFPVALSCRCGPCRLSSSDCGGPRAQPLACDRP 135


RESULT 8
LSHB_HORSE
ID   LSHB_HORSE     STANDARD;      PRT;   169 AA.
AC   P08751; P01234;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lutropin/choriogonadotropin beta chain precursor (LSH-B/CG-B)
DE   (Lutenizing hormone beta subunit).
GN   LHB.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92357035; PubMed=1379674;
RA   Sherman G.B., Wolfe M.W., Farmerie T.A., Clay C.M.,
RA   Threadgill D.S., Sharp D.C., Nilson J.H.;
RT   "A single gene encodes the beta-subunits of equine luteinizing
RT   hormone and chorionic gonadotropin.";
RL   Mol. Endocrinol. 6:951-959(1992).
RN   [2]
RP   SEQUENCE OF 21-169.
RX   MEDLINE=87250476; PubMed=3298239;
RA   Bousfield G.R., Liu W.-K., Sugino H., Ward D.N.;
RT   "Structural studies on equine glycoprotein hormones. Amino acid
RT   sequence of equine lutropin beta-subunit.";
RL   J. Biol. Chem. 262:8610-8620(1987).
RN   [3]
RP   SEQUENCE OF 21-169.
RX   MEDLINE=87250475; PubMed=3298238;
RA   Sugino H., Bousfield G.R., Moore W.T. Jr., Ward D.N.;
RT   "Structural studies on equine glycoprotein hormones. Amino acid
RT   sequence of equine chorionic gonadotropin beta-subunit.";
RL   J. Biol. Chem. 262:8603-8609(1987).
RN   [4]
RP   PARTIAL SEQUENCE.
RA   Ward D.N., Moore W.T. Jr., Burleigh B.D.;
RT   "Structural studies on equine chorionic gonadotropin.";
RL   J. Protein Chem. 1:263-280(1982).
RN   [5]
RP   STRUCTURE OF CARBOHYDRATES.
RX   MEDLINE=90235854; PubMed=2331995;
RA   Damm J.B.L., Haard K., Kamerling J.P., van Dedem G.W.K.,
RA   Vliegenthart J.F.G.;
RT   "Structure determination of the major N- and O-linked carbohydrate
RT   chains of the beta subunit from equine chorionic gonadotropin.";
RL   Eur. J. Biochem. 189:175-183(1990).
RN   [6]
RP   O-GLYCOSYLATION.
RX   PubMed=11133668;
RA   Bousfield G.R., Butnev V.Y., Butnev V.Y.;
RT   "Identification of twelve O-glycosylation sites in equine chorionic
RT   gonadotropin beta and equine luteinizing hormone beta by solid-phase
RT   Edman degradation.";
RL   Biol. Reprod. 64:136-147(2001).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- PTM: MICROHETEROGENEITY AT ASN-33. O-GLYCOSYLATION APPEARS TO BE
CC       RESPONSIBLE FOR THE BETA SUBUNIT CONTRIBUTION TO THE DIFFERENCE IN
CC       LH RECEPTOR-BINDING ACTIVITY BETWEEN LSH-B AND CG-B.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; S41704; AAB22775.1; -.
DR   PIR; A01503; KTHOB.
DR   PIR; A29304; A29304.
DR   PIR; A29305; A29305.
DR   PIR; A41917; A41917.
DR   HSSP; P01233; 1XUL.
DR   GlycoSuiteDB; P08751; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Glycoprotein; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    169       LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    138    138       O-LINKED (GALNAC. . .).
FT   CARBOHYD    143    143       O-LINKED (GALNAC. . .).
FT   CARBOHYD    147    147       O-LINKED (GALNAC. . .).
FT   CARBOHYD    148    148       O-LINKED (GALNAC. . .).
FT   CARBOHYD    149    149       O-LINKED (GALNAC. . .).
FT   CARBOHYD    150    150       O-LINKED (GALNAC. . .).
FT   CARBOHYD    151    151       O-LINKED (GALNAC. . .).
FT   CARBOHYD    153    153       O-LINKED (GALNAC. . .).
FT   CARBOHYD    157    157       O-LINKED (GALNAC. . .).
FT   CARBOHYD    160    160       O-LINKED (GALNAC. . .).
FT   CARBOHYD    161    161       O-LINKED (GALNAC. . .).
FT   CARBOHYD    169    169       O-LINKED (GALNAC. . .).
SQ   SEQUENCE   169 AA;  17865 MW;  1244ADBEB843EF1A CRC64;

  Query Match             33.0%;  Score 444;  DB 1;  Length 169;
  Best Local Similarity   57.7%;  Pred. No. 4.2e-30;
  Matches   86;  Conservative   16;  Mismatches   39;  Indels    8;  Gaps    2;

Qy    103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
          |||| |||||||||| ||| ||:|||  |:||||||:| ||:   |||:|| || ||::|
Db     24 PLRPLCRPINATLAAEKEACPICITFTTSICAGYCPSMVRVMPAALPAIPQPVCTYRELR 83

Qy    163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKA 222
          | |||||||| ||:|:||: ||||| |  |:  ||||| :| || |     | |||||
Db     84 FASIRLPGCPPGVDPMVSFPVALSCHCGPCQIKTTDCGVFRDQPLACAP---QASSSSKD 140

Qy    223 PPPSLPSPSRLPGP-----SDTPILPQTS 246
          ||    : :  | |     |  |:  :||
Db    141 PPSQPLTSTSTPTPGASRRSSHPLPIKTS 169


RESULT 9
LSHB_BOVIN
ID   LSHB_BOVIN     STANDARD;      PRT;   141 AA.
AC   P04651;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE   beta) (LSH-B) (LH-B).
GN   LHB.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85207729; PubMed=2987241;
RA   Virgin J.B., Silver B.J., Thomason A.R., Nilson J.H.;
RT   "The gene for the beta subunit of bovine luteinizing hormone encodes
RT   a gonadotropin mRNA with an unusually short 5'-untranslated region.";
RL   J. Biol. Chem. 260:7072-7077(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85182575; PubMed=3838746;
RA   Maurer R.A.;
RT   "Analysis of several bovine lutropin beta subunit cDNAs reveals
RT   heterogeneity in nucleotide sequence.";
RL   J. Biol. Chem. 260:4684-4687(1985).
RN   [3]
RP   SEQUENCE OF 21-139.
RX   MEDLINE=74075724; PubMed=4770795;
RA   Maghuin-Rogister G., Hennen G.;
RT   "Luteinizing hormone. The primary structures of the beta-subunit from
RT   bovine and porcine species.";
RL   Eur. J. Biochem. 39:235-253(1973).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; M10077; AAA30623.1; -.
DR   EMBL; M11506; AAB59267.1; -.
DR   PIR; A01499; UTBOB.
DR   HSSP; P01233; 1XUL.
DR   GlycoSuiteDB; P04651; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .).
FT                                /FTId=CAR_000044.
FT   CONFLICT      1      2       MISSING (IN REF. 2).
FT   CONFLICT     74     74       Q -> E (IN REF. 3).
FT   CONFLICT    112    112       P -> S (IN REF. 2).
FT   CONFLICT    122    123       GP -> PG (IN REF. 3).
FT   CONFLICT    126    126       Q -> E (IN REF. 3).
SQ   SEQUENCE   141 AA;  15202 MW;  44FB1CBD4901BC95 CRC64;
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  Query Match             32.3%;  Score 435;  DB 1;  Length 141;
  Best Local Similarity   65.8%;  Pred. No. 1.9e-29;
  Matches   75;  Conservative   13;  Mismatches   26;  Indels    0;  Gaps    0;

Qy     103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
           |||| |:||||||| ||| ||||||  |:||||||:| |||  :|| :|| || | ::|
Db      24 PLRPLCQPINATLAAEKEACPVCITFTTSICAGYCPSMKRVLPVILPPMPQRVCTYHELR 83

Qy     163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQD 216
           | |:|||||| ||:|:||: ||||| |  || |:|||||:  || || |   |
Db      84 FASVRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDHPPLPD 137


RESULT 10
LSHB_RAT
ID   LSHB_RAT       STANDARD;      PRT;   141 AA.
AC   P01230;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE   beta) (LSH-B) (LH-B).
GN   LHB.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=83273673; PubMed=6192440;
RA   Chin W.W., Godine J.E., Klein D.R., Chang A.S., Tan L.K.,
RA   Habener J.F.;
RT   "Nucleotide sequence of the cDNA encoding the precursor of the beta
RT   subunit of rat lutropin.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4649-4653(1983).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85080043; PubMed=6096374;
RA   Jameson L., Chin W.W., Hollenberg A.N., Chang A.S., Habener J.F.;
RT   "The gene encoding the beta-subunit of rat luteinizing hormone.
RT   Analysis of gene structure and evolution of nucleotide sequence.";
RL   J. Biol. Chem. 259:15474-15480(1984).
RN   [3]
RP   SEQUENCE OF 4-141 FROM N.A.
RC   STRAIN=Wistar Imamichi; TISSUE=Anterior pituitary;
RA   Kato Y., Ezashi T., Hirai T., Kato T.;
RT   "Strain difference in nucleotide sequences of rat glycoprotein hormone
RT   subunit cDNAs and gene fragment.";
RL   Zool. Sci. 7:877-885(1990).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; V01542; CAA24783.1; -.
DR   EMBL; J00749; AAA96703.1; -.
DR   EMBL; D00576; BAA00454.1; -.
DR   PIR; A01498; UTRTB.
DR   PIR; S42527; S42527.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL       1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29    77        BY SIMILARITY.
FT   DISULFID     43    92        BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     113   120       BY SIMILARITY.
FT   CARBOHYD     33    33        N-LINKED (GLCNAC. . .) (PROBABLE).
SQ   SEQUENCE   141 AA;  15177 MW;  50796FB8E32F83BF CRC64;

  Query Match             32.1%;  Score 432;  DB 1;  Length 141;
  Best Local Similarity   66.4%;  Pred. No. 3.4e-29;
  Matches   73;  Conservative   15;  Mismatches   22;  Indels    0;  Gaps    0;

Qy     103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
           |||| |||:||||| | | ||||||  |:||||||:| |||   || :|| || ||::|
Db      24 PLRPLCRPVNATLAAENEFCPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELR 83

Qy     163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 212
           | |:|||||| ||:|:||: |||||:|  || |::|||||:  |:||| |
Db      84 FASVRLPGCPPGVDPIVSFPVALSCRCGPCRLSSSDCGGPRTQPMTCDLP 133


RESULT 11
MFA1_SACBA
ID   MFA1_SACBA     STANDARD;      PRT;   144 AA.
AC   P25501;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Mating factor alpha precursor (Alpha mating pheromone).
OS   Saccharomyces bayanus (Yeast) (Saccharomyces uvarum).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4931;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IFO 0751;
RX   MEDLINE=88194702; PubMed=2834101;
RA   Kitada K., Hishinuma F.;
RT   "Evidence for preferential multiplication of the internal unit in
RT   tandem repeats of the mating factor alpha genes in Saccharomyces
RT   yeasts.";
RL   Curr. Genet. 13:1-5(1988).
CC   -!- FUNCTION: THE ACTIVE FACTOR IS EXCRETED INTO THE CULTURE MEDIUM BY
CC       HAPLOID CELLS OF THE ALPHA MATING TYPE AND ACTS ON CELLS OF THE
CC       OPPOSITE MATING TYPE (TYPE A). IT MEDIATES THE CONJUGATION PROCESS
CC       BETWEEN THE TWO TYPES BY INHIBITING THE INITIATION OF DNA
CC       SYNTHESIS IN TYPE A CELLS AND SYNCHRONIZING THEM WITH TYPE ALPHA.
CC   -!- SIMILARITY: THE MATING FACTOR ALPHA-1 PRECURSOR IS IDENTICAL IN
CC       S.ITALICUS, S.UVARUM AND S.CEREVISIAE, EXCEPT FOR THE NUMBER OF
CC       TANDEM REPEAT UNITS: 5, 3 AND 4 RESPECTIVELY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M55013; AAA34813.1; -.
KW   Pheromone; Cleavage on pair of basic residues; Repeat; Signal.
FT   SIGNAL       1     19        OR 20 (PROBABLE).
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FT   CHAIN        20    144       ALPHA-1 MATING PHEROMONE.
FT   PEPTIDE      90    102       MATING FACTOR ALPHA (1ST COPY).
FT   PEPTIDE     111    123       MATING FACTOR ALPHA (2ND COPY).
FT   PEPTIDE     132    144       MATING FACTOR ALPHA (3RD COPY).
SQ   SEQUENCE   144 AA;  16091 MW;  97E3C2B8AA98F996 CRC64;

  Query Match             31.9%;  Score 429.5;  DB 1;  Length 144;
  Best Local Similarity   83.5%;  Pred. No. 5.6e-29;
  Matches   91;  Conservative    6;  Mismatches    5;  Indels    7;  Gaps    2;

Qy       1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSNSTN 60
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYLDLEGDFDVAVLPFSNSTN 60

Qy      61 NGLLFINTTIASIAAKEEGVSLEKREAEA--YVEFDPGCRDLKEPLRPR 107
           ||||||||||||||||||||:||||||  :::  ||     :|:  |
Db      61 NGLLFINTTIASIAAKEEGVSLDKREAEAWHWLQLKPG-----QPMYKR 104


RESULT 12
MFA3_YEAST
ID   MFA3_YEAST     STANDARD;      PRT;   165 AA.
AC   P01149;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-APR-1988 (Rel. 07, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Mating factor alpha-1 precursor (Alpha-1 mating pheromone) [Contains:
DE   Mating factor alpha].
GN   MFAL1 OR MF-ALPHA-1 OR YPL187W.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83246532; PubMed=6306574;
RA   Singh A., Chen E.Y., Lugovoy J.M., Chang C.N., Hitzeman R.A.,
RA   Seeburg P.H.;
RT   "Saccharomyces cerevisiae contains two discrete genes coding for the
RT   alpha-factor pheromone.";
RL   Nucleic Acids Res. 11:4049-4063(1983).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83050979; PubMed=6754095;
RA   Kurjan J., Herskowitz I.;
RT   "Structure of a yeast pheromone gene (MF alpha): a putative
RT   alpha-factor precursor contains four tandem copies of mature
RT   alpha-factor.";
RL   Cell 30:933-943(1982).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c / AB972;
RX   MEDLINE=97313271; PubMed=9169875;
RA   Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W.,
RA   Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
RA   Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
RA   Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
RA   Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,
RA   Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
RA   Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,
RA   Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,
RA   Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
RA   Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
RA   Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
RA   Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M.,
RA   Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,
RA   Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,
RA   Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,
RA   Zhong W.W., Zollner A., Vo D.H., Hani J.;
RT   "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
RL   Nature 387:103-105(1997).
RN   [4]
RP   SEQUENCE OF 1-9 FROM N.A.
RX   MEDLINE=88038871; PubMed=2959859;
RA   Inokuchi K., Nakayama A., Hishinuma F.;
RT   "Identification of sequence elements that confer cell-type-specific
RT   control of MF alpha 1 expression in Saccharomyces cerevisiae.";
RL   Mol. Cell. Biol. 7:3185-3193(1987).
RN   [5]
RP   SEQUENCE OF THE ACTIVE FACTOR.
RA   Stoetzler D., Kiltz H.-H., Duntze W.;
RT   "Primary structure of alpha-factor peptides from Saccharomyces
RT   cerevisiae.";
RL   Eur. J. Biochem. 69:397-400(1976).
RN   [6]
RP   SEQUENCE OF THE ACTIVE FACTOR.
RX   MEDLINE=78087498; PubMed=340452;
RA   Tanaka T., Kita H., Murakami T., Narita K.;
RT   "Purification and amino acid sequence of mating factor from
RT   Saccharomyces cerevisiae.";
RL   J. Biochem. 82:1681-1687(1977).
CC   -!- FUNCTION: THE ACTIVE FACTOR IS EXCRETED INTO THE CULTURE MEDIUM BY
CC       HAPLOID CELLS OF THE ALPHA MATING TYPE AND ACTS ON CELLS OF THE
CC       OPPOSITE MATING TYPE (TYPE A). IT MEDIATES THE CONJUGATION PROCESS
CC       BETWEEN THE TWO TYPES BY INHIBITING THE INITIATION OF DNA
CC       SYNTHESIS IN TYPE A CELLS AND SYNCHRONIZING THEM WITH TYPE ALPHA.
CC   -!- SIMILARITY: THE MATING FACTOR ALPHA-1 PRECURSOR IS IDENTICAL IN
CC       S.ITALICUS, S.UVARUM AND S.CEREVISIAE, EXCEPT FOR THE NUMBER OF
CC       TANDEM REPEAT UNITS: 5, 3 AND 4 RESPECTIVELY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X01581; CAA25734.1; -.
DR   EMBL; X01581; CAA25735.1; ALT_SEQ.
DR   EMBL; X01581; CAA25736.1; ALT_SEQ.
DR   EMBL; X01581; CAA25737.1; ALT_SEQ.
DR   EMBL; X01581; CAA25738.1; ALT_SEQ.
DR   EMBL; J01340; AAA88727.1; -.
DR   EMBL; Z73543; CAA97899.1; -.
DR   EMBL; M17301; AAA34777.1; -.
DR   EMBL; A14990; CAA01206.1; -.
DR   PIR; A01413; JFBY1.
DR   SGD; S0006108; MF(ALPHA)1.
KW   Pheromone; Cleavage on pair of basic residues; Repeat; Signal.
FT   SIGNAL        1     19       OR 20 (PROBABLE).
FT   CHAIN        20    165       ALPHA-1 MATING PHEROMONE.
FT   PEPTIDE      90    102       MATING FACTOR ALPHA (1ST COPY).
FT   PEPTIDE     111    123       MATING FACTOR ALPHA (2ND COPY).
FT   PEPTIDE     132    144       MATING FACTOR ALPHA (3RD COPY).
FT   PEPTIDE     153    165       MATING FACTOR ALPHA (4TH COPY).
FT   CONFLICT     42     42       L -> S (IN REF. 2).
SQ   SEQUENCE   165 AA;  18642 MW;  826ACB932DE3D128 CRC64;

  Query Match             31.9%;  Score 429.5;  DB 1;  Length 165;
  Best Local Similarity   83.5%;  Pred. No. 6.6e-29;
  Matches   91;  Conservative    6;  Mismatches    5;  Indels    7;  Gaps    2;

Qy       1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSNSTN 60
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYLDLEGDFDVAVLPFSNSTN 60

Qy      61 NGLLFINTTIASIAAKEEGVSLEKREAEA--YVEFDPGCRDLKEPLRPR 107
           ||||||||||||||||||||:||||||  :::  ||     :|:  |
Db      61 NGLLFINTTIASIAAKEEGVSLDKREAEAWHWLQLKPG-----QPMYKR 104


RESULT 13
MFA1_YEAST
ID   MFA1_YEAST     STANDARD;      PRT;   186 AA.
AC   P25041;
```

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DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Mating factor alpha precursor (Alpha mating pheromone).
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Italicus / IFO 0253;
RX   MEDLINE=88194702; PubMed=2834101;
RA   Kitada K., Hishinuma F.;
RT   "Evidence for preferential multiplication of the internal unit in
RT   tandem repeats of the mating factor alpha genes in Saccharomyces
RT   yeasts.";
RL   Curr. Genet. 13:1-5(1988).
CC   -!- FUNCTION: THE ACTIVE FACTOR IS EXCRETED INTO THE CULTURE MEDIUM BY
CC       HAPLOID CELLS OF THE ALPHA MATING TYPE AND ACTS ON CELLS OF THE
CC       OPPOSITE MATING TYPE (TYPE A). IT MEDIATES THE CONJUGATION PROCESS
CC       BETWEEN THE TWO TYPES BY INHIBITING THE INITIATION OF DNA
CC       SYNTHESIS IN TYPE A CELLS AND SYNCHRONIZING THEM WITH TYPE ALPHA.
CC   -!- SIMILARITY: THE MATING FACTOR ALPHA-1 PRECURSOR IS IDENTICAL IN
CC       S.ITALICUS, S.UVARUM AND S.CEREVISIAE, EXCEPT FOR THE NUMBER OF
CC       TANDEM REPEAT UNITS: 5, 3 AND 4 RESPECTIVELY.
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M55016; AAA34778.1; -.
KW   Pheromone; Cleavage on pair of basic residues; Repeat; Signal.
FT   SIGNAL        1     19       OR 20 (PROBABLE).
FT   CHAIN        20    186       ALPHA-1 MATING PHEROMONE.
FT   PEPTIDE      90    102       MATING FACTOR ALPHA (1ST COPY).
FT   PEPTIDE     111    123       MATING FACTOR ALPHA (2ND COPY).
FT   PEPTIDE     132    144       MATING FACTOR ALPHA (3RD COPY).
FT   PEPTIDE     153    165       MATING FACTOR ALPHA (4TH COPY).
FT   PEPTIDE     174    186       MATING FACTOR ALPHA (5TH COPY).
SQ   SEQUENCE   186 AA;  21165 MW;  8F014F9EE263D8CF CRC64;

  Query Match             31.9%;  Score 429.5;  DB 1;  Length 186;
  Best Local Similarity   83.5%;  Pred. No. 7.6e-29;
  Matches   91;  Conservative    6;  Mismatches    5;  Indels    7;  Gaps    2;

Qy       1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSNSTN 60
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYLDLEGDFDVAVLPFSNSTN 60

Qy      61 NGLLFINTTIASIAAKEEGVSLEKREAEA--YVEFDPGCRDLKEPLRPR 107
           ||||||||||||||||||:|||||  :::  ||     :|:  |
Db      61 NGLLFINTTIASIAAKEEGVSLDKREAEAWHWLQLKPG-----QPMYKR 104


RESULT 14
LSHB_CERSI
ID   LSHB_CERSI     STANDARD;      PRT;   141 AA.
AC   O77835; O19102;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE   beta) (LSH-B) (LH-B).
GN   LHB1 AND LHB2.
OS   Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
OX   NCBI_TaxID=9807;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98389253; PubMed=9723860;
RA   Lund L.A., Sherman G.B.;
RT   "Duplication of the southern white rhinoceros (Ceratotherium simum
RT   simum) luteinizing hormone beta subunit gene.";
RL   J. Mol. Endocrinol. 21:19-30(1998).
RN   [2]
RP   SEQUENCE OF 7-141 FROM N.A.
RC   TISSUE=Pituitary;
RX   MEDLINE=97449288; PubMed=9305757;
RA   Sherman G.B., Lund L.A., Bunick D., Winn R.J.;
RT   "Characterization and phylogenetic significance of rhinoceros
RT   luteinizing hormone beta (LHbeta) subunit messenger RNA structure,
RT   complementary DNA sequence and gene copy number.";
RL   Gene 195:131-139(1997).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF024521; AAC36049.1; -.
DR   EMBL; AF024520; AAC36048.1; -.
DR   EMBL; U72659; AAB71983.1; -.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     20       BY SIMILARITY.
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     22     22       R -> K (IN REF. 2).
SQ   SEQUENCE   141 AA;  14930 MW;  FFEDB157C51976C9 CRC64;

  Query Match             31.6%;  Score 426;  DB 1;  Length 141;
  Best Local Similarity   67.3%;  Pred. No. 1.1e-28;
  Matches   74;  Conservative   11;  Mismatches   25;  Indels    0;  Gaps    0;

Qy     103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
           |||| |||||||||  | | ||||||  |:|||||||:| |||   ||  || || | ::|
Db      24 PLRPLCRPINATLAAENEACPVCITFTTSICAGYCPSMVRVLPAALPPAPQPVCTYHELR 83

Qy     163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 212
           | |||||||| ||:|:||: |||||:|  || |::|||||:  || || |
Db      84 FASIRLPGCPPGVDPMVSFPVALSCRCGPCRLSSSDCGGPRAQPLACDRP 133


RESULT 15
LSHB_PIG
ID   LSHB_PIG       STANDARD;      PRT;   141 AA.
AC   P01232;
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DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE   beta) (LSH-B) (LH-B).
GN   LHB.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91063934; PubMed=1701088;
RA   Ezashi T., Hirai T., Kato T., Wakabayashi K., Kato Y.;
RT   "The gene for the beta subunit of porcine LH: clusters of GC boxes
RT   and CACCC elements.";
RL   J. Mol. Endocrinol. 5:137-146(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89306142; PubMed=2744222;
RA   Kato Y., Hirai T.;
RT   "Cloning and DNA sequence analysis of the cDNA for the precursor of
RT   porcine luteinizing hormone (LH) beta subunit.";
RL   Mol. Cell. Endocrinol. 62:47-53(1989).
RN   [3]
RP   SEQUENCE OF 21-139.
RX   MEDLINE=74075724; PubMed=4770795;
RA   Maghuin-Rogister G., Hennen G.;
RT   "Luteinizing hormone. The primary structures of the beta-subunit from
RT   bovine and porcine species.";
RL   Eur. J. Biochem. 39:235-253(1973).
CC   -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC       THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC   -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC       CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC       LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC   -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC       FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D00579; BAA00457.1; -.
DR   PIR; A30322; UTPGB.
DR   PIR; A48170; A48170.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     20
FT   CHAIN        21    141       LUTROPIN BETA CHAIN.
FT   DISULFID     29     77       BY SIMILARITY.
FT   DISULFID     43     92       BY SIMILARITY.
FT   DISULFID     46    130       BY SIMILARITY.
FT   DISULFID     54    108       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID    113    120       BY SIMILARITY.
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .).
FT   MOD_RES      21     21       BLOCKED.
FT   VARIANT      30     30       R -> Z.
FT   CONFLICT     40     40       N -> D (IN REF. 3).
FT   CONFLICT     62     62       V -> R (IN REF. 3).
FT   CONFLICT     83     83       S -> I (IN REF. 3).
FT   CONFLICT     87     87       I -> S (IN REF. 3).
FT   CONFLICT    122    123       GP -> PG (IN REF. 3).
SQ   SEQUENCE   141 AA;  14889 MW;  803E8E7C59F3C2CF CRC64;

  Query Match             31.6%;  Score 425;  DB 1;  Length 141;
  Best Local Similarity   67.3%;  Pred. No. 1.3e-28;
  Matches   74;  Conservative   10;  Mismatches   26;  Indels    0;  Gaps    0;

Qy    103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
          |||| |||||||||| | | ||||||  |:||||||:| |||   || :|| || ||::
Db     24 PLRPLCRPINATLAAENEACPVCITFTTSICAGYCPSMVRVLPAALPPVPQPVCTYRELS 83

Qy    163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDP 212
          | |||||||| ||:| ||: |||| |  || |::|||||:  || || |
Db     84 FASIRLPGCPPGVDPTVSFPVALSCHCGPCRLSSSDCGGPRAQPLACDRP 133


Search completed: November 20, 2002, 17:27:59
Job time : 10.986 secs
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us-09-787-494-4.rspt

Thu Nov 21 06:11:42 2002

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:27 ; Search time 31.1329 Seconds
(without alignments)
1667.815 Million cell updates/sec

Title: US-09-787-494-4
Perfect score: 1347
Sequence: 1 MRFPSIFTAVLFAASSALAA.....LPGPSDTPILPQTSHHHHHH 252

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	788	58.5	159	4	Q8WTT5	Q8wtt5 homo sapien
2	783	58.1	159	4	Q8WXL2	Q8wxl2 homo sapien
3	776	57.6	159	4	Q8WXL3	Q8wxl3 homo sapien
4	764	56.7	159	4	Q8WXL4	Q8wxl4 homo sapien
5	758	56.3	159	4	Q8WXL1	Q8wxl1 homo sapien
6	737	54.7	157	6	Q8WNC4	Q8wnc4 pongo pygma
7	735	54.6	157	6	Q8WNC7	Q8wnc7 pongo pygma
8	735	54.6	157	6	Q8WNC5	Q8wnc5 pongo pygma
9	726	53.9	157	6	Q8WNC6	Q8wnc6 pongo pygma
10	657	48.8	165	6	Q9BEH1	Q9beh1 macaca fasc
11	654	48.6	159	6	Q8WNB0	Q8wnb0 macaca mula
12	653	48.5	159	6	Q8WNA9	Q8wna9 macaca mula
13	652	48.4	165	6	Q9BEH2	Q9beh2 macaca fasc
14	646	48.0	159	6	Q8WNB2	Q8wnb2 colobus gue
15	646	48.0	159	6	Q8WNA8	Q8wna8 macaca mula
16	644	47.8	159	6	Q8WNB1	Q8wnb1 colobus gue
17	642	47.7	165	6	Q9GL37	Q9gl37 macaca mula
18	642	47.7	165	11	Q99P48	Q99p48 mus musculu
19	631	46.8	159	6	Q8WNB3	Q8wnb3 colobus gue
20	628	46.6	159	6	Q8WNB4	Q8wnb4 colobus gue
21	616	45.7	157	6	Q8WNB9	Q8wnb9 presbytis o
22	615	45.7	157	6	Q8WNC3	Q8wnc3 presbytis o
23	609	45.2	157	6	Q8WNC0	Q8wnc0 presbytis o
24	607	45.1	157	6	Q8WNC1	Q8wnc1 presbytis o
25	605	44.9	157	6	Q8WNC2	Q8wnc2 presbytis o
26	574	42.6	136	6	Q8WNB8	Q8wnb8 pongo pygma
27	540	40.1	136	4	Q8WXL0	Q8wxl0 homo sapien
28	515	38.2	136	6	Q8WNB6	Q8wnb6 presbytis o
29	505	37.5	136	6	Q8WNB5	Q8wnb5 colobus gue
30	498.5	37.0	156	6	Q8WNA6	Q8wna6 aotus trivi
31	498	37.0	136	6	Q8WNB7	Q8wnb7 macaca mula
32	476.5	35.4	156	6	Q8WNA7	Q8wna7 callicebus
33	444	33.0	142	6	Q9BDI9	Q9bdi9 panthera ti
34	441	32.7	136	6	Q8WNA5	Q8wna5 tarsius ban
35	436	32.4	136	6	Q8WNA2	Q8wna2 galago sene
36	435	32.3	136	6	Q8WNA4	Q8wna4 daubentonia
37	432	32.1	136	6	Q8WNA3	Q8wna3 lemur varie
38	431	32.0	136	6	Q8WNA0	Q8wna0 cynocephalu
39	431	32.0	139	11	Q62778	Q62778 rattus norv
40	431	32.0	141	6	Q8WN18	Q8wn18 ailuropoda
41	427	31.7	136	6	Q8WNA1	Q8wna1 loris tardi
42	413	30.7	136	6	Q8WN99	Q8wn99 pteropus ly
43	411	30.5	86	3	Q02436	Q02436 saccharomyc
44	396	29.4	127	11	Q924A6	Q924a6 cavia porce
45	396	29.4	135	11	Q924A7	Q924a7 cavia porce

ALIGNMENTS

RESULT 1
Q8WTT5 PRELIMINARY; PRT; 159 AA.
ID Q8WTT5
AC Q8WTT5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
RT evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF397577; AAL69705.1; -.
DR EMBL; AF397580; AAL69708.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 1
FT NON_TER 159 159
SQ SEQUENCE 159 AA; 16944 MW; 246BA938796A1727 CRC64;

Query Match 58.5%; Score 788; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.1e-67;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 17 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 76

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Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220

Qy     221 KAPPPSLPSPSRLPGPSDTPILP 243
           |||||||||||||||||||||||
Db     137 KAPPPSLPSPSRLPGPSDTPILP 159


RESULT 2
Q8WXL2
ID   Q8WXL2       PRELIMINARY;      PRT;   159 AA.
AC   Q8WXL2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397579; AAL69707.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER      1      1
FT   NON_TER    159    159
SQ   SEQUENCE   159 AA;  16960 MW;  24761E38796A1727 CRC64;

  Query Match             58.1%;  Score 783;  DB 4;  Length 159;
  Best Local Similarity   99.3%;  Pred. No. 6.3e-67;
  Matches  142;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220

Qy     221 KAPPPSLPSPSRLPGPSDTPILP 243
           ||||| ||||||||||||||||||
Db     137 KAPPPCLPSPSRLPGPSDTPILP 159


RESULT 3
Q8WXL3
ID   Q8WXL3       PRELIMINARY;      PRT;   159 AA.
AC   Q8WXL3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397578; AAL69706.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER      1      1
FT   NON_TER    159    159
SQ   SEQUENCE   159 AA;  17006 MW;  AFDC4CE2542EC084 CRC64;

  Query Match             57.6%;  Score 776;  DB 4;  Length 159;
  Best Local Similarity   98.6%;  Pred. No. 2.9e-66;
  Matches  141;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
           :| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17 REMLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220

Qy     221 KAPPPSLPSPSRLPGPSDTPILP 243
           |||||||||||||||||||||||
Db     137 KAPPPSLPSPSRLPGPSDTPILP 159


RESULT 4
Q8WXL4
ID   Q8WXL4       PRELIMINARY;      PRT;   159 AA.
AC   Q8WXL4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397576; AAL69704.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER      1      1
FT   NON_TER    159    159
SQ   SEQUENCE   159 AA;  16909 MW;  A598A73CC97B57EE CRC64;

  Query Match             56.7%;  Score 764;  DB 4;  Length 159;
  Best Local Similarity   97.2%;  Pred. No. 4.1e-65;
  Matches  139;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
           :|||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17 REPLRPWCHPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220

Qy     221 KAPPPSLPSPSRLPGPSDTPILP 243
           |||||||||||||||||||||||
Db     137 KAPPPSLPSPSRLPGPSDTPILP 159
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          ||||||||||||||||||||||
Db    137 KAPPPSLPSPSRLPGPSDTPILP 159


RESULT 5
Q8WXL1
ID   Q8WXL1      PRELIMINARY;      PRT;   159 AA.
AC   Q8WXL1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397581; AAL69709.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     159    159
SQ   SEQUENCE   159 AA;  16969 MW;  3C963B3C3D2E57FF CRC64;

  Query Match             56.3%;  Score 758;  DB 4;  Length 159;
  Best Local Similarity   96.5%;  Pred. No. 1.5e-64;
  Matches  138;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
          :||||| | |||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     17 REPLRPWCHPINAILAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 76

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     77 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGTKDHPLTCDDPRFQDSSSS 136

Qy    221 KAPPPSLPSPSRLPGPSDTPILP 243
          |||||||||||||||||||||||
Db    137 KAPPPSLPSPSRLPGPSDTPILP 159


RESULT 6
Q8WNC4
ID   Q8WNC4      PRELIMINARY;      PRT;   157 AA.
AC   Q8WNC4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397585; AAL69713.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     157    157
SQ   SEQUENCE   157 AA;  16985 MW;  825D27AC3EFBD4F6 CRC64;

  Query Match             54.7%;  Score 737;  DB 6;  Length 157;
  Best Local Similarity   95.0%;  Pred. No. 1.5e-62;
  Matches  133;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
          |||||||||||||||||||||||:||||||||||||||||| ||| ||||||||||
Db     17 KEPLRPRCRPINATLAVEKEGCPVCVTVNTTICAGYCPTMTRVLQSVLPPLPQVVCNYRD 76

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     77 VRFEYIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDPSSS 136

Qy    221 KAPPPSLPSPSRLPGPSDTP 240
          |||||||||||||| ||:||
Db    137 KAPPPSLPSPSRLPEPSNTP 156


RESULT 7
Q8WNC7
ID   Q8WNC7      PRELIMINARY;      PRT;   157 AA.
AC   Q8WNC7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397582; AAL69710.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     157    157
SQ   SEQUENCE   157 AA;  16928 MW;  825D27A00EFBD4F6 CRC64;

  Query Match             54.6%;  Score 735;  DB 6;  Length 157;
  Best Local Similarity   95.0%;  Pred. No. 2.4e-62;
  Matches  133;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
          |||||||||||||||||||||||:||||||||||||||||| ||| ||||||||||
Db     17 KEPLRPRCRPINATLAVEKEGCPVCVTVNTTICAGYCPTMTRVLQSVLPPLPQVVCNYRD 76

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     77 VRFEYIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDPSSS 136

Qy    221 KAPPPSLPSPSRLPGPSDTP 240
          |||||||||||||| || ||
Db    137 KAPPPSLPSPSRLPEPSGTP 156


RESULT 8
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Q8WNC5
ID   Q8WNC5       PRELIMINARY;      PRT;   157 AA.
AC   Q8WNC5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397584; AAL69712.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     157    157
SQ   SEQUENCE   157 AA;  17027 MW;  8317774E0F4BD4ED CRC64;

  Query Match             54.6%;  Score 735;  DB 6;  Length 157;
  Best Local Similarity   95.0%;  Pred. No. 2.4e-62;
  Matches  133;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
           |||||||||||||||||||||||||||:||||||||||||||||||| ||| ||||||||||
Db      17 KEPLRPRCRPINATLAVEKEGCPVCVTVNTTICAGYCPTMTRVLQSVLPPLPQVVCNYRD 76

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
           |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77 VRFEYIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDPSSS 136

Qy     221 KAPPPSLPSPSRLPGPSDTP 240
           ||||||||||||| || ||
Db     137 KAPPPSLPSPSRLPEPSGTP 156


RESULT 9
Q8WNC6
ID   Q8WNC6       PRELIMINARY;      PRT;   157 AA.
AC   Q8WNC6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN.  CGB.
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397583; AAL69711.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     157    157
SQ   SEQUENCE   157 AA;  16868 MW;  97BD27A014E1D4EC CRC64;

  Query Match             53.9%;  Score 726;  DB 6;  Length 157;
  Best Local Similarity   94.3%;  Pred. No. 1.7e-61;
  Matches  132;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
           |||||||||||||||||||||||||||:||||||||||||||||||| ||| ||||||||||
Db      17 KEPLRPRCRPINATLAVEKEGCPVCVTVNTTICAGYCPTMTRVLQSVLPPLPQVVCNYRD 76

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
           |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77 VRFEYIRLPGCPRGVNPVVSCAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDPSSS 136

Qy     221 KAPPPSLPSPSRLPGPSDTP 240
           ||||||||||||| || ||
Db     137 KAPPPSLPSPSRLPEPSGTP 156


RESULT 10
Q9BEH1
ID   Q9BEH1       PRELIMINARY;      PRT;   165 AA.
AC   Q9BEH1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Chorionic gonadotropin beta subunit 2.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EMBRYONIC TROPHOBLAST;
RA   Wilken J.A., Matsumoto K., Lasley B.L., Bedows E.;
RT   "A Comparison of Chorionic Gonadotropin Expression by Human and
RT   Macaque Trophoblast Cells.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY026360; AAK08644.1; -.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
SQ   SEQUENCE   165 AA;  17743 MW;  2F21566B48592471 CRC64;

  Query Match             48.8%;  Score 657;  DB 6;  Length 165;
  Best Local Similarity   80.5%;  Pred. No. 7e-55;
  Matches  120;  Conservative    7;  Mismatches   22;  Indels    0;  Gaps    0;

Qy      96 GCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVV 155
           | |  :||||| |||||||| ||| |||||||||||||||||| |||| ||| :||||
Db      17 GARASREPLRPLCRPINATLAAEKEACPVCITVNTTICAGYCPTMMRVLQAVLPPVPQVV 76

Qy     156 CNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQ 215
           ||||:||||||||||| ||:|||| |||||:| ||||||:|||||||||||||| |
Db      77 CNYREVRFESIRLPGCPPGVDPVVSVPVALSCRCGLCRRSTSDCGGPKDHPLTCDDPHLQ 136

Qy     216 DSSSSKAPPPSLPSPSRLPGPSDTPILPQ 244
           ||||| |||| |||||| |:| | |||
Db     137 ASSSSKDPPPSPPSPSRLLEPADNPFLPQ 165


RESULT 11
Q8WNB0
ID   Q8WNB0       PRELIMINARY;      PRT;   159 AA.
AC   Q8WNB0;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
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DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397600; AAL69728.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     159    159
SQ   SEQUENCE   159 AA;  16853 MW;  7B64051C2F863870 CRC64;

  Query Match             48.6%;  Score 654;  DB 6;  Length 159;
  Best Local Similarity   81.1%;  Pred. No. 1.3e-54;
  Matches  120;  Conservative    7;  Mismatches   21;  Indels    0;  Gaps    0;

Qy      96 GCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVV 155
           | |  :|||||  |||||||||  ||| ||||||||||||||||||| |||| ||| :||||
Db      12 GARASREPLRPLCRPINATLAAEKEACPVCITVNTTICAGYCPTMMRVLQAVLPPVPQVV 71

Qy     156 CNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQ 215
           ||||:||||||||||| ||:|||| |||||:||||||||:|||||||||||||||  |
Db      72 CNYREVRFESIRLPGCPPGVDPVVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPHLQ 131

Qy     216 DSSSSKAPPPSLPSPSRLPGPSDTPILP 243
             ||||| |||| |||| |  |:||| ||
Db     132 ASSSSKDPPPSPPSPSGLLEPADTPFLP 159


RESULT 12
Q8WNA9
ID   Q8WNA9      PRELIMINARY;      PRT;   159 AA.
AC   Q8WNA9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397601; AAL69729.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     159    159
SQ   SEQUENCE   159 AA;  16915 MW;  9231691ED0D82863 CRC64;

  Query Match             48.5%;  Score 653;  DB 6;  Length 159;
  Best Local Similarity   80.4%;  Pred. No. 1.6e-54;
  Matches  119;  Conservative    9;  Mismatches   20;  Indels    0;  Gaps    0;

Qy      96 GCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVV 155
           | :  :|||:| |||||||| ||| ||||||||||||||||| |||| ||| :||||
Db      12 GAQASREPLQPLCRPINATLAAEKEACPVCITVNTTICAGYCPTMMRVLQAVLPPVPQVV 71

Qy     156 CNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQ 215
           ||||:||||||||||| ||:|||| |||||:||||||||:|||||||||||||||  |
Db      72 CNYREVRFESIRLPGCPPGVDPVVSVPVALSCRCALCRRSTSDCGGPKDHPLTCDDPHLQ 131

Qy     216 DSSSSKAPPPSLPSPSRLPGPSDTPILP 243
             ||||| |||| |||||| |:||| ||
Db     132 ASSSSKDPPPSPPSPSRLLEPADTPFLP 159


RESULT 13
Q9BEH2
ID   Q9BEH2      PRELIMINARY;      PRT;   165 AA.
AC   Q9BEH2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Chorionic gonadotropin beta subunit 1.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EMBRYONIC TROPHOBLAST;
RA   Wilken J.A., Matsumoto K., Lasley B.L., Bedows E.;
RT   "A Comparison of Chorionic Gonadotropin Expression by Human and
RT   Macaque Trophoblast Cells.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY026359; AAK08643.1; -.
DR   HSSP; P01233; 1XUL.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
SQ   SEQUENCE   165 AA;  17711 MW;  280DF602157D9940 CRC64;

  Query Match             48.4%;  Score 652;  DB 6;  Length 165;
  Best Local Similarity   79.9%;  Pred. No. 2.1e-54;
  Matches  119;  Conservative    8;  Mismatches   22;  Indels    0;  Gaps    0;

Qy      96 GCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVV 155
           | |  :|||||  |||||||||  ||| ||||||||||||||||||| |||  :|| :||||
Db      17 GARASREPLRPLCRPINATLAAEKEACPVCITVNTTICAGYCPTMMRVLPVILPPVPQVV 76

Qy     156 CNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQ 215
           ||||:||||||||||| ||:|||| |||||:| ||||||:|||||||||||||||  |
Db      77 CNYREVRFESIRLPGCPPGVDPVVSVPVALSCRCGLCRRSTSDCGGPKDHPLTCDDPHLQ 136

Qy     216 DSSSSKAPPPSLPSPSRLPGPSDTPILPQ 244
             ||||| |||| ||||||  |:||| |||
Db     137 ASSSSKDPPPSPPSPSRLLEPADTPFLPQ 165


RESULT 14
Q8WNB2
ID   Q8WNB2      PRELIMINARY;      PRT;   159 AA.
AC   Q8WNB2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
```

```
OS   Colobus guereza (Black-and-white colobus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Colobus.
OX   NCBI_TaxID=33548;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397598; AAL69726.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     159    159
SQ   SEQUENCE   159 AA;  16972 MW;  725BA76BC2887660 CRC64;

  Query Match             48.0%;  Score 646;  DB 6;  Length 159;
  Best Local Similarity   81.8%;  Pred. No. 7.5e-54;
  Matches  117;  Conservative    7;  Mismatches   19;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
           :||||| |||||||| ||| ||||||||||||||||||| |||| ||| :|| |||||:
Db      17 REPLRPLCRPINATLAAEKEACPVCITVNTTICAGYCPTMMRVLQAVLPPVPQAVCNYRE 76

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
           |||||||||||| ||:|||| |||||:| |||||:|||||||||||||||  | ||||
Db      77 VRFESIRLPGCPPGVDPVVSIPVALSCRCGLCRRSTSDCGGPKDHPLTCDDPHLQASSSS 136

Qy     221 KAPPPSLPSPSRLPGPSDTPILP 243
           | |||||||||||  |: || ||
Db     137 KDPPPSLPSPSRLLEPAGTPFLP 159


RESULT 15
Q8WNA8
ID   Q8WNA8      PRELIMINARY;      PRT;   159 AA.
AC   Q8WNA8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Chorionic gonadotropin beta subunit (Fragment).
GN   CGB.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maston G.A., Ruvolo M.;
RT   "Chorionic gonadotropin has a recent origin in primates and an
RT   evolutionary history of selection.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF397602; AAL69730.1; -.
DR   InterPro; IPR000359; Cys_knot.
DR   InterPro; IPR001545; Gly_hormoneB.
DR   Pfam; PF00007; Cys_knot; 1.
DR   SMART; SM00068; GHB; 1.
DR   PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR   PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     159    159
SQ   SEQUENCE   159 AA;  17032 MW;  726E29F7A27E5C04 CRC64;

  Query Match             48.0%;  Score 646;  DB 6;  Length 159;
  Best Local Similarity   80.8%;  Pred. No. 7.5e-54;
  Matches  118;  Conservative    8;  Mismatches   20;  Indels    0;  Gaps    0;

Qy      98 RDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCN 157
           |  :||||| |||||||| ||| |||||||||||||||||| |||| :|| :||||||
Db      14 RASREPLRPLCRPINATLAAEKEACPVCITVNTTICAGYCPTMMRVLQVILPPVPQVVCN 73

Qy     158 YRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDS 217
           ||:||||||||||| ||:|||| |||||:|||||||:|||||||||| ||||  | |
Db      74 YREVRFESIRLPGCPPGVDPVVSVPVALSCRCALCRRSTSDCGGPKDHPLACDDPHLQAS 133

Qy     218 SSSKAPPPSLPSPSRLPGPSDTPILP 243
           |||| |||| |||||| |:||| ||
Db     134 SSSKDPPPSPPSPSRLLEPADTPFLP 159


Search completed: November 20, 2002, 17:28:59
Job time : 31.1329 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:21 ; Search time 38.1818 Seconds
(without alignments)
879.454 Million cell updates/sec

Title: US-09-787-494-4
Perfect score: 1347
Sequence: 1 MRFPSIFTAVLFAASSALAA.....LPGPSDTPILPQTSHHHHHH 252

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
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2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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19: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1347	100.0	252	21	AAY57316	Alpha-mating facto
2	886.5	65.8	176	21	AAY57315	Human betahCG/beta
3	804	59.7	273	20	AAY43292	HCG beta subunit-J
4	802	59.5	273	20	AAY43285	HCG beta subunit-J
5	795	59.0	209	20	AAY43299	HCG beta subunit-J
6	795	59.0	212	20	AAY43304	HCG beta subunit-J
7	795	59.0	265	22	AAU04602	Single chain gonad
8	795	59.0	265	22	AAU04614	Single chain gonad
9	795	59.0	265	22	AAE04474	Human single chain
10	795	59.0	265	22	AAE04486	Human single chain
11	793	58.9	145	20	AAW93434	Human hCG beta-sub
12	793	58.9	145	20	AAW95520	Human chorionic go
13	793	58.9	145	21	AAB20558	Human chorionic go
14	793	58.9	145	22	AAU04619	Human chorionic go
15	793	58.9	145	22	AAE04491	Human chorionic go
16	793	58.9	145	22	AAU00709	Beta-subunit of Hu
17	793	58.9	145	22	AAU01139	Human chorionic go
18	793	58.9	145	22	AAB71765	Beta-human chorion
19	793	58.9	145	22	AAB04121	Beta subunit of hu
20	793	58.9	145	23	AAM50776	Human chorionic go
21	793	58.9	145	23	AAU83014	Beta-human chorion
22	793	58.9	165	12	AAR15043	Human chorionic go
23	793	58.9	165	20	AAY05748	Human chorionic go
24	793	58.9	165	20	AAW99533	Human chorionic go
25	793	58.9	165	21	AAB15358	Human chorionic go
26	793	58.9	165	22	AAB49896	Human chorionic go
27	793	58.9	165	23	AAU96134	Human chorionic go
28	793	58.9	203	20	AAY43298	HCG beta subunit-J
29	793	58.9	206	20	AAY43303	HCG beta subunit-J
30	791.5	58.8	212	20	AAY43278	Human CG beta subu
31	790	58.6	165	19	AAW47473	Human beta-hCG pro
32	790	58.6	165	19	AAW33639	Human chorionic go
33	790	58.6	165	19	AAW33637	Human chorionic go
34	789	58.6	145	20	AAW99530	Human chorionic go
35	789	58.6	165	20	AAW99508	Glycoprotein hormo
36	789	58.6	181	22	AAU04613	Gonadotropin analo
37	789	58.6	181	22	AAE04485	Human single chain
38	788.5	58.5	144	12	AAR15178	hCG histidine subs
39	788	58.5	145	12	AAR15171	hCG methionine sub
40	788	58.5	145	12	AAR15173	hCG histidine subs
41	788	58.5	165	20	AAW99514	Glycoprotein hormo
42	788	58.5	165	20	AAW99507	Glycoprotein hormo
43	788	58.5	165	20	AAW99509	Glycoprotein hormo
44	787	58.4	145	12	AAR15169	hCG methionine sub
45	787	58.4	145	14	AAR30999	Human chorionic go

ALIGNMENTS

RESULT 1
AAY57316
ID AAY57316 standard; Protein; 252 AA.
XX
AC AAY57316;
XX
DT 19-JUN-2000 (first entry)
XX
DE Alpha-mating factor fragment/betahCG fusion protein.
XX
KW Human chorionic gonadotropin; hCG; betahCG; vaccine; chitosan;
KW infertility; betahCG/beta-gal; fusion protein.
XX
OS Homo sapiens.
XX
PN WO200015253-A1.
XX
PD 23-MAR-2000.
XX
PF 16-SEP-1999; 99WO-US21591.
XX
PR 17-SEP-1998; 98US-0100766.
XX
PA (ZONA-) ZONAGEN INC.
XX
PI Harris J, Martinez M;
XX
DR WPI; 2000-271258/23.
DR N-PSDB; AAZ90610.
XX
PT Novel human beta-subunit chorionic gonadotropin vaccines used to
PT interrupt fertility in mammals by the immunological inactivation of the
PT pregnancy hormone chorionic gonadotropin -

XX
PS Claim 5; Page 34-35; 39pp; English.
XX
CC The invention provides novel vaccine compositions which comprise the
CC beta-subunit of human chorionic gonadotropin (betahCG)in combination
CC with chitosan-based adjuvants. The vaccines are used to induce
CC infertility especially transient infertility, in female mammals. The
CC compositions are also used for antibody production. The vaccines comprise
CC a well-tolerated chitosan-based adjuvant which induces the production of
CC anti-chorionic gonadotropin antibodies, without inducing the side effects
CC (e.g. hypersensitivity, erythema, etc.) associated with other adjuvants.
CC The vaccine also overcomes the problem of non-responsiveness in some
CC individuals. The present sequence represents a betahCG fragment
CC fused to an alpha-mating factor leader sequence at the N-terminus.
XX
SQ Sequence 252 AA;

Query Match 100.0%; Score 1347; DB 21; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.1e-104;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSNSTN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSNSTN 60

Qy     61 NGLLFINTTIASIAAKEEGVSLEKREAEAYVEFDPGCRDLKEPLRPRCRPINATLAVEKE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NGLLFINTTIASIAAKEEGVSLEKREAEAYVEFDPGCRDLKEPLRPRCRPINATLAVEKE 120

Qy    121 GCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVS 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVS 180

Qy    181 YAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTP 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 YAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTP 240

Qy    241 ILPQTSHHHHHH 252
          ||||||||||||
Db    241 ILPQTSHHHHHH 252
```

RESULT 2
AAY57315
ID AAY57315 standard; Protein; 176 AA.
XX
AC AAY57315;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human betahCG/beta-gal fusion protein.
XX
KW Human chorionic gonadotropin; hCG; betahCG; vaccine; chitosan;
KW infertility; betahCG/beta-gal; fusion protein.
XX
OS Homo sapiens.
XX
PN WO200015253-A1.
XX
PD 23-MAR-2000.
XX
PF 16-SEP-1999; 99WO-US21591.
XX
PR 17-SEP-1998; 98US-0100766.
XX
PA (ZONA-) ZONAGEN INC.
XX
PI Harris J, Martinez M;
XX
DR WPI; 2000-271258/23.
DR N-PSDB; AAZ90609.
XX
PT Novel human beta-subunit chorionic gonadotropin vaccines used to
PT interrupt fertility in mammals by the immunological inactivation of the
PT pregnancy hormone chorionic gonadotropin -
XX
PS Claim 5; Page 32-33; 39pp; English.
XX
CC The invention provides novel vaccine compositions which comprise the
CC beta-subunit of human chorionic gonadotropin (betahCG)in combination
CC with chitosan-based adjuvants. The vaccines are used to induce
CC infertility especially transient infertility, in female mammals. The
CC compositions are also used for antibody production. The vaccines comprise
CC a well-tolerated chitosan-based adjuvant which induces the production of
CC anti-chorionic gonadotropin antibodies, without inducing the side effects
CC (e.g. hypersensitivity, erythema, etc.) associated with other adjuvants.
CC The vaccine also overcomes the problem of non-responsiveness in some
CC individuals. The present sequence represents a betahCG/beta-gal fusion
CC protein consisting of leaderless betahCG linked to a beta-gal fragment.
XX
SQ Sequence 176 AA;

Query Match 65.8%; Score 886.5; DB 21; Length 176;
Best Local Similarity 93.6%; Pred. No. 2.2e-66;
Matches 161; Conservative 4; Mismatches 2; Indels 5; Gaps 1;

```
Qy     80 VSLEKREAEAYVEFDPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPT 139
          | |::|: |     :||||||||||||||||||||||||||||||||||||||||||||||
Db     10 VVLQRRDWE-----NPGCRDLKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPT 64

Qy    140 MTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     65 MTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDC 124

Qy    200 GGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQTSHHHHH 251
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 GGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQTSHHHHH 176
```

RESULT 3
AAY43292
ID AAY43292 standard; Protein; 273 AA.
XX
AC AAY43292;
XX
DT 19-JAN-2000 (first entry)
XX
DE HCG beta subunit-Jun fusion protein sequence.
XX
KW Cysteine knot protein; protein formation; heterodimeric protein analog;
KW deglycosylated glycoprotein hormone; infertility; immunogen; antigen;
KW polycystic ovarian disease; hCG; human; chorionic gonadotrophin;
KW beta subunit; therapy; Jun.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9953065-A1.
XX
PD 21-OCT-1999.
XX
PF 13-APR-1999; 99WO-US08018.
XX
PR 14-APR-1998; 98US-0059625.
XX
PA (UYNE-) UNIV NEW JERSEY.
XX
PI Moyle WR;
XX
DR WPI; 1999-620431/53.
XX
PT Methods for producing heterodimers, particularly analogues of hormones,
PT from subunits of cysteine knot proteins -
XX
PS Example 6; Fig 19; 73pp; English.
XX

```
CC   This sequence is a fusion protein of HCG and Jun. The invention
CC   relates to a method of forming a cysteine knot protein (I) having alpha
CC   and beta-subunits comprising attaching a dimerisation domain (DD) to
CC   either the N-termini of both subunits or the N-terminus of the
CC   alpha-subunit and to the C-terminus of the beta-subunit and dimerising
CC   the products to form a heterodimeric protein analog (II). The method is
CC   used to produce analogues (agonists or antagonists) of deglycosylated
CC   glycoprotein hormones, potentially useful, e.g. for treating infertility
CC   where caused by polycystic ovarian disease (associated with excessive
CC   levels of luteinising hormone). Products that retain DD's are also useful
CC   as immunogens or antigens (since a DD may containing highly antigenic
CC   amino acid sequences). Attachment of a DD (which may be removed later)
CC   facilitates the formation of heterodimers, that have similar structures
CC   (and thus receptor-binding and immunogenic properties) to native dimers,
CC   and allows the combination of subunits that would otherwise combine
CC   poorly, or not at all. The N-terminal part of a glycoprotein hormone may
CC   be modified without loss of activity, and attachment of the DD reduces
CC   formation of homodimers. Heterodimers have longer circulation times in
CC   vivo than individual subunits.
XX
SQ   Sequence   273 AA;

  Query Match             59.7%;  Score 804;  DB 20;  Length 273;
  Best Local Similarity   65.0%;  Pred. No. 2.8e-59;
  Matches  158;  Conservative   15;  Mismatches   26;  Indels   44;  Gaps    4;

Qy       3 FPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSNSTNNG 62
           ||::  : |:  ||::  |        ::  |:|
Db      74 FPAVLESDLYTLSSSVTVP--------SSPRPSE------------------------- 99

Qy      63 LLFINTTIASIAAKEEGVSLEKREAEAYVEFDPG-CRDLKEPLRPRCRPINATLAVEKEG 121
             .|   ::|       ::|:     |  | |  :  ||||||||||||||||||||
Db     100 -----TVTCNVAHPASSTKVDKK----IVPRDAGKSKRSKEPLRPRCRPINATLAVEKEG 150

Qy     122 CPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSY 181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151 CPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSY 210

Qy     182 AVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPI 241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     211 AVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPI 270

Qy     242 LPQ 244
           |||
Db     271 LPQ 273


RESULT 4
AAY43285
ID   AAY43285 standard; Protein; 273 AA.
XX
AC   AAY43285;
XX
DT   19-JAN-2000  (first entry)
XX
DE   HCG beta subunit-Jun fusion protein sequence.
XX
KW   Cysteine knot protein; protein formation; heterodimeric protein analog;
KW   deglycosylated glycoprotein hormone; infertility; immunogen; antigen;
KW   polycystic ovarian disease; hCG; human; chorionic gonadotrophin;
KW   beta subunit; therapy; Jun.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9953065-A1.
XX
PD   21-OCT-1999.
XX
PF   13-APR-1999;   99WO-US08018.
XX
PR   14-APR-1998;   98US-0059625.
XX
PA   (UYNE-) UNIV NEW JERSEY.
XX
PI   Moyle WR;
XX
DR   WPI; 1999-620431/53.
XX
PT   Methods for producing heterodimers, particularly analogues of hormones,
PT   from subunits of cysteine knot proteins -
XX
PS   Example 6; Fig 18; 73pp; English.
XX
CC   This sequence is a fusion protein of hCG and Jun. The invention
CC   relates to a method of forming a cysteine knot protein (I) having alpha
CC   and beta-subunits comprising attaching a dimerisation domain (DD) to
CC   either the N-termini of both subunits or the N-terminus of the
CC   alpha-subunit and to the C-terminus of the beta-subunit and dimerising
CC   the products to form a heterodimeric protein analog (II). The method is
CC   used to produce analogues (agonists or antagonists) of deglycosylated
CC   glycoprotein hormones, potentially useful, e.g. for treating infertility
CC   where caused by polycystic ovarian disease (associated with excessive
CC   levels of luteinising hormone). Products that retain DD's are also useful
CC   as immunogens or antigens (since a DD may containing highly antigenic
CC   amino acid sequences). Attachment of a DD (which may be removed later)
CC   facilitates the formation of heterodimers, that have similar structures
CC   (and thus receptor-binding and immunogenic properties) to native dimers,
CC   and allows the combination of subunits that would otherwise combine
CC   poorly, or not at all. The N-terminal part of a glycoprotein hormone may
CC   be modified without loss of activity, and attachment of the DD reduces
CC   formation of homodimers. Heterodimers have longer circulation times in
CC   vivo than individual subunits.
XX
SQ   Sequence   273 AA;

  Query Match             59.5%;  Score 802;  DB 20;  Length 273;
  Best Local Similarity   65.0%;  Pred. No. 4.1e-59;
  Matches  158;  Conservative   15;  Mismatches   26;  Indels   44;  Gaps    4;

Qy       3 FPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSNSTNNG 62
           ||::  : |:  ||::  |        ::  |:|
Db      74 FPAVLESDLYTLSSSVTVP--------SSPRPSE------------------------- 99

Qy      63 LLFINTTIASIAAKEEGVSLEKREAEAYVEFDPG-CRDLKEPLRPRCRPINATLAVEKEG 121
             |   ::|       ::|:     |  | |  :  ||||||||||||||||||||
Db     100 -----TVTCNVAHPASSTKVDKK----IVPRDCGKSKRSKEPLRPRCRPINATLAVEKEG 150

Qy     122 CPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSY 181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151 CPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSY 210

Qy     182 AVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPI 241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     211 AVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPI 270

Qy     242 LPQ 244
           |||
Db     271 LPQ 273


RESULT 5
AAY43299
ID   AAY43299 standard; Protein; 209 AA.
XX
AC   AAY43299;
XX
DT   19-JAN-2000  (first entry)
XX
DE   HCG beta subunit-Jun fusion protein sequence.
XX
KW   Cysteine knot protein; protein formation; heterodimeric protein analog;
KW   deglycosylated glycoprotein hormone; infertility; immunogen; antigen;
KW   polycystic ovarian disease; hCG; human; chorionic gonadotrophin;
KW   beta subunit; therapy; Jun.
XX
```

OS Homo sapiens.
OS Synthetic.
XX
PN WO9953065-A1.
XX
PD 21-OCT-1999.
XX
PF 13-APR-1999; 99WO-US08018.
XX
PR 14-APR-1998; 98US-0059625.
XX
PA (UYNE-) UNIV NEW JERSEY.
XX
PI Moyle WR;
XX
DR WPI; 1999-620431/53.
XX
PT Methods for producing heterodimers, particularly analogues of hormones,
PT from subunits of cysteine knot proteins -
XX
PS Example 7; Fig 20; 73pp; English.
XX
CC This sequence is a fusion protein of HCG and Jun. The invention
CC relates to a method of forming a cysteine knot protein (I) having alpha
CC and beta-subunits comprising attaching a dimerisation domain (DD) to
CC either the N-termini of both subunits or the N-terminus of the
CC alpha-subunit and to the C-terminus of the beta-subunit and dimerising
CC the products to form a heterodimeric protein analog (II). The method is
CC used to produce analogues (agonists or antagonists) of deglycosylated
CC glycoprotein hormones, potentially useful, e.g. for treating infertility
CC where caused by polycystic ovarian disease (associated with excessive
CC levels of luteinising hormone). Products that retain DD's are also useful
CC as immunogens or antigens (since a DD may containing highly antigenic
CC amino acid sequences). Attachment of a DD (which may be removed later)
CC facilitates the formation of heterodimers, that have similar structures
CC (and thus receptor-binding and immunogenic properties) to native dimers,
CC and allows the combination of subunits that would otherwise combine
CC poorly, or not at all. The N-terminal part of a glycoprotein hormone may
CC be modified without loss of activity, and attachment of the DD reduces
CC formation of homodimers. Heterodimers have longer circulation times in
CC vivo than individual subunits.
XX
SQ Sequence 209 AA;

Query Match 59.0%; Score 795; DB 20; Length 209;
Best Local Similarity 99.3%; Pred. No. 1.2e-58;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy 161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy 221 KAPPPSLPSPSRLPGPSDTPILPQTS 246
||||||||||||||||||||||||| |
Db 142 KAPPPSLPSPSRLPGPSDTPILPQGS 167

RESULT 6
AAY43304
ID AAY43304 standard; Protein; 212 AA.
XX
AC AAY43304;
XX
DT 19-JAN-2000 (first entry)
XX
DE HCG beta subunit-Jun fusion protein sequence.
XX
KW Cysteine knot protein; protein formation; heterodimeric protein analog;
KW deglycosylated glycoprotein hormone; infertility; immunogen; antigen;
KW polycystic ovarian disease; hCG; human; chorionic gonadotrophin;
KW beta subunit; therapy; Jun.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9953065-A1.
XX
PD 21-OCT-1999.
XX
PF 13-APR-1999; 99WO-US08018.
XX
PR 14-APR-1998; 98US-0059625.
XX
PA (UYNE-) UNIV NEW JERSEY.
XX
PI Moyle WR;
XX
DR WPI; 1999-620431/53.
XX
PT Methods for producing heterodimers, particularly analogues of hormones,
PT from subunits of cysteine knot proteins -
XX
PS Example 7; Fig 20; 73pp; English.
XX
CC This sequence is a fusion protein of HCG and Jun. The invention
CC relates to a method of forming a cysteine knot protein (I) having alpha
CC and beta-subunits comprising attaching a dimerisation domain (DD) to
CC either the N-termini of both subunits or the N-terminus of the
CC alpha-subunit and to the C-terminus of the beta-subunit and dimerising
CC the products to form a heterodimeric protein analog (II). The method is
CC used to produce analogues (agonists or antagonists) of deglycosylated
CC glycoprotein hormones, potentially useful, e.g. for treating infertility
CC where caused by polycystic ovarian disease (associated with excessive
CC levels of luteinising hormone). Products that retain DD's are also useful
CC as immunogens or antigens (since a DD may containing highly antigenic
CC amino acid sequences). Attachment of a DD (which may be removed later)
CC facilitates the formation of heterodimers, that have similar structures
CC (and thus receptor-binding and immunogenic properties) to native dimers,
CC and allows the combination of subunits that would otherwise combine
CC poorly, or not at all. The N-terminal part of a glycoprotein hormone may
CC be modified without loss of activity, and attachment of the DD reduces
CC formation of homodimers. Heterodimers have longer circulation times in
CC vivo than individual subunits.
XX
SQ Sequence 212 AA;

Query Match 59.0%; Score 795; DB 20; Length 212;
Best Local Similarity 99.3%; Pred. No. 1.2e-58;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy 161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy 221 KAPPPSLPSPSRLPGPSDTPILPQTS 246
||||||||||||||||||||||||| |
Db 142 KAPPPSLPSPSRLPGPSDTPILPQGS 167

RESULT 7
AAU04602
ID AAU04602 standard; Protein; 265 AA.
XX
AC AAU04602;
XX
DT 23-OCT-2001 (first entry)
XX
DE Single chain gonadotropin analogue #1.

XX
KW Human; glycoprotein hormone; infertility; in vivo fertilisation;
KW single chain gonadotropin.
XX
OS Homo sapiens.
XX
PN US6242580-B1.
XX
PD 05-JUN-2001.
XX
PF 31-MAR-1999; 99US-0282357.
XX
PR 25-AUG-1997; 97US-0918288.
PR 18-FEB-1994; 94US-0199382.
PR 12-AUG-1994; 94US-0289396.
PR 22-SEP-1994; 94US-0310590.
PR 04-NOV-1994; 94US-0334628.
PR 07-DEC-1994; 94US-0351591.
PR 07-JUN-1995; 95US-0475049.
PR 09-MAY-1997; 97US-0853524.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Boime I, Moyle WR;
XX
DR WPI; 2001-424301/45.
DR N-PSDB; AAS08485.
XX
PT New single chain forms of the glycoprotein hormone quartet useful for
PT generating antibodies specifically immunoreactive with the new
PT compounds, in treating infertility, or as aids for in vivo
PT fertilization techniques -
XX
PS Example 5; Fig 5; 86pp; English.
XX
CC The sequence represents the amino acid sequence of single chain
CC gonadotropin analogue #1. The glycoprotein hormone analogue is
CC useful for generating antibodies specifically immunoreactive with new
CC compounds, as a substitute for the heterodimeric forms of the hormones,
CC in the treatment of infertility, as an aid for in vivo fertilisation
CC techniques, and in other therapeutic methods associated with the native
CC hormone. The single chain protein is further useful as a reagent in a
CC manner similar to the heterodimer, as a diagnostic tool to detect the
CC presence of antibodies with respect to the native proteins in the
CC biological samples, as a control reagent in assay kits for assessing the
CC levels of these hormones in various samples, and in detecting and
CC purifying receptors to which the native hormones bind. The single chain
CC forms of the heterodimers or homodimers have the following advantages
CC over their dimeric forms: they are more stable, problems of recombinant
CC production are reduced since only a single gene is needed to transcribe,
CC translate and process, provide an alternate form thus permitting fine
CC tuning of activity levels and of in vivo half lives. Single chain forms
CC are unique starting materials for identifying truncated forms with the
CC activity of the dimer. The linkage between the subunits permits the
CC protein to be engineered without disturbing the overall folding of the
CC protein.
XX
SQ Sequence 265 AA;

Query Match 59.0%; Score 795; DB 22; Length 265;
Best Local Similarity 99.3%; Pred. No. 1.5e-58;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy 161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy 221 KAPPPSLPSPSRLPGPSDTPILPQTS 246
|||||||||||||||||||||||| |
Db 142 KAPPPSLPSPSRLPGPSDTPILPQGS 167

RESULT 8
AAU04614
ID AAU04614 standard; Protein; 265 AA.
XX
AC AAU04614;
XX
DT 23-OCT-2001 (first entry)
XX
DE Single chain gonadotropin analogue #1a.
XX
KW Human; glycoprotein hormone; infertility; in vivo fertilisation;
KW single chain gonadotropin.
XX
OS Homo sapiens.
XX
PN US6242580-B1.
XX
PD 05-JUN-2001.
XX
PF 31-MAR-1999; 99US-0282357.
XX
PR 25-AUG-1997; 97US-0918288.
PR 18-FEB-1994; 94US-0199382.
PR 12-AUG-1994; 94US-0289396.
PR 22-SEP-1994; 94US-0310590.
PR 04-NOV-1994; 94US-0334628.
PR 07-DEC-1994; 94US-0351591.
PR 07-JUN-1995; 95US-0475049.
PR 09-MAY-1997; 97US-0853524.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Boime I, Moyle WR;
XX
DR WPI; 2001-424301/45.
DR N-PSDB; AAS08509.
XX
PT New single chain forms of the glycoprotein hormone quartet useful for
PT generating antibodies specifically immunoreactive with the new
PT compounds, in treating infertility, or as aids for in vivo
PT fertilization techniques -
XX
PS Example 16; Fig 17; 86pp; English.
XX
CC The sequence represents the amino acid sequence of single chain
CC gonadotropin analogue #1a. The glycoprotein hormone analogue is
CC useful for generating antibodies specifically immunoreactive with new
CC compounds, as a substitute for the heterodimeric forms of the hormones,
CC in the treatment of infertility, as an aid for in vivo fertilisation
CC techniques, and in other therapeutic methods associated with the native
CC hormone. The single chain protein is further useful as a reagent in a
CC manner similar to the heterodimer, as a diagnostic tool to detect the
CC presence of antibodies with respect to the native proteins in the
CC biological samples, as a control reagent in assay kits for assessing the
CC levels of these hormones in various samples, and in detecting and
CC purifying receptors to which the native hormones bind. The single chain
CC forms of the heterodimers or homodimers have the following advantages
CC over their dimeric forms: they are more stable, problems of recombinant
CC production are reduced since only a single gene is needed to transcribe,
CC translate and process, provide an alternate form thus permitting fine
CC tuning of activity levels and of in vivo half lives. Single chain forms
CC are unique starting materials for identifying truncated forms with the
CC activity of the dimer. The linkage between the subunits permits the
CC protein to be engineered without disturbing the overall folding of the
CC protein.
XX
SQ Sequence 265 AA;

Query Match 59.0%; Score 795; DB 22; Length 265;
Best Local Similarity 99.3%; Pred. No. 1.5e-58;

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  Matches  145;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy     221 KAPPPSLPSPSRLPGPSDTPILPQTS 246
           |||||||||||||||||||||||||  |
Db     142 KAPPPSLPSPSRLPGPSDTPILPQGS 167


RESULT 9
AAE04474
ID   AAE04474 standard; Protein; 265 AA.
XX
AC   AAE04474;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human single chain gonadotropin analog no:1.
XX
KW   Human; single chain gonadotropin analog no:1; anti-infertility; drug;
KW   peptide therapy; luteinising hormone; LH; follicle stimulating hormone;
KW   FSH; thyroid stimulating hormone; TSH; chorionic gonadotropin; CG;
KW   glycoprotein; infertility; fusion protein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          21..165
FT                   /note= "Corresponds to 1-145 amino acids of human
FT                   chorionic gonadotropin (CG) beta-subunit"
FT   Region          166..173
FT                   /note= "Linker peptide"
FT   Region          174..265
FT                   /note= "Corresponds to 1-92 amino acids of human single
FT                   chain gonadotropin alpha-subunit"
XX
PN   US6238890-B1.
XX
PD   29-MAY-2001.
XX
PF   25-AUG-1997;   97US-0918288.
XX
PR   18-FEB-1994;   94US-0199382.
PR   12-AUG-1994;   94US-0289396.
PR   22-SEP-1994;   94US-0310590.
PR   04-NOV-1994;   94US-0334628.
PR   07-DEC-1994;   94US-0351591.
PR   07-JUN-1995;   95US-0475049.
PR   09-MAY-1997;   97US-0853524.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Boime I,  Moyle WR;
XX
DR   WPI; 2001-366474/38.
DR   N-PSDB; AAD08785.
XX
PT   New DNA or RNA encoding single chain protein useful in treating
PT   infertility, as aids in vitro fertilization techniques, or other
PT   therapeutic methods associated with the native hormones
XX
PS   Claim 9; Fig 5; 87pp; English.
XX
CC   The invention relates to human single chain forms of the glycoprotein
CC   hormone quartet which is an agonist or antagonist of luteinising hormone
CC   (LH), follicle stimulating hormone (FSH), thyroid stimulating hormone
CC   (TSH) or chorionic gonadotropin (CG). All these hormones are heterodimers
CC   having identical alpha subunits and differing beta subunits. The agonist
CC   forms of single chain hormones are used in treating infertility, as aids
CC   in vitro fertilisation techniques, and other therapeutic methods
CC   associated with the native hormones. The single chain hormones are useful
CC   as reagents in a manner similar to heterodimers, as diagnostic tools to
CC   detect the presence of antibodies with respect to the native proteins in
CC   biological samples, as control reagents in assay kits for assessing the
CC   levels of these hormones in various samples, in detecting and purifying
CC   receptors to which the native hormones bind. The single chain hormones
CC   are also used in affinity chromatographic preparation of receptors or
CC   antihormone antibodies. They are used as purification tools for
CC   isolation of subsequent preparations of these materials and to monitor
CC   levels of single chain hormones administered as drugs. The single chain
CC   glycoproteins are used to generate antibodies specifically immunoreactive
CC   with these new compounds, as substitutes for the heterodimeric forms of
CC   hormones. The present sequence is human single chain gonadotropin analog
CC   no:1 related to the invention. Analog no:1 is a fusion protein consisting
CC   of human chorionic gonadotropin (CG) beta-subunit (1-145 amino acids)
CC   fused to human single chain gonadotropin alpha-subunit (1-92 amino acids)
CC   by a linker sequence. This analog serves as a useful starting compound
CC   for template directed vaccine design and for the development of hormone-
CC   specific vaccines for use in humans.
XX
SQ   Sequence   265 AA;

  Query Match             59.0%;  Score 795;  DB 22;  Length 265;
  Best Local Similarity   99.3%;  Pred. No. 1.5e-58;
  Matches  145;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy     221 KAPPPSLPSPSRLPGPSDTPILPQTS 246
           |||||||||||||||||||||||||  |
Db     142 KAPPPSLPSPSRLPGPSDTPILPQGS 167


RESULT 10
AAE04486
ID   AAE04486 standard; Protein; 265 AA.
XX
AC   AAE04486;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human single chain gonadotropin analog no:1a.
XX
KW   Human; single chain gonadotropin analog no:1a; anti-infertility; drug;
KW   peptide therapy; luteinising hormone; LH; follicle stimulating hormone;
KW   FSH; thyroid stimulating hormone; TSH; chorionic gonadotropin; CG;
KW   glycoprotein; infertility; fusion protein; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          21..165
FT                   /note= "Corresponds to 1-145 amino acids of human
FT                   chorionic gonadotropin (CG) beta-subunit"
FT   Region          166..173
FT                   /note= "Linker peptide"
FT   Region          174..265
FT                   /note= "Corresponds to 1-92 amino acids of human single
FT                   chain gonadotropin alpha-subunit"
FT   Misc-difference 225
FT.                  /note= "Wild type Asn substituted with Gln"
FT   Misc-difference 251
```

```
FT                   /note= "Wild type Asn substituted with Gln"
XX
PN   US6238890-B1.
XX
PD   29-MAY-2001.
XX
PF   25-AUG-1997;   97US-0918288.
XX
PR   18-FEB-1994;   94US-0199382.
PR   12-AUG-1994;   94US-0289396.
PR   22-SEP-1994;   94US-0310590.
PR   04-NOV-1994;   94US-0334628.
PR   07-DEC-1994;   94US-0351591.
PR   07-JUN-1995;   95US-0475049.
PR   09-MAY-1997;   97US-0853524.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Boime I,  Moyle WR;
XX
DR   WPI; 2001-366474/38.
DR   N-PSDB; AAD08809.
XX
PT   New DNA or RNA encoding single chain protein useful in treating
PT   infertility, as aids in vitro fertilization techniques, or other
PT   therapeutic methods associated with the native hormones  -
XX
PS   Claim 9; Fig 17; 87pp; English.
XX
CC   The invention relates to human single chain forms of the glycoprotein
CC   hormone quartet which is an agonist or antagonist of luteinising hormone
CC   (LH), follicle stimulating hormone (FSH), thyroid stimulating hormone
CC   (TSH) or chorionic gonadotropin (CG). All these hormones are heterodimers
CC   having identical alpha subunits and differing beta subunits. The agonist
CC   forms of single chain hormones are used in treating infertility, as aids
CC   in vitro fertilisation techniques, and other therapeutic methods
CC   associated with the native hormones. The single chain hormones are useful
CC   as reagents in a manner similar to heterodimers, as diagnostic tools to
CC   detect the presence of antibodies with respect to the native proteins in
CC   biological samples, as control reagents in assay kits for assessing the
CC   levels of these hormones in various samples, in detecting and purifying
CC   receptors to which the native hormones bind. The single chain hormones
CC   are also used in affinity chromatographic preparation of receptors or
CC   antihormone antibodies. They are used as purification tools for
CC   isolation of subsequent preparations of these materials and to monitor
CC   levels of single chain hormones administered as drugs. The single chain
CC   glycoproteins are used to generate antibodies specifically immunoreactive
CC   with these new compounds, as substitutes for the heterodimeric forms of
CC   hormones. The present sequence is human single chain gonadotropin analog
CC   no:1a related to the invention. Analog no:1a is a fusion protein
CC   consisting of human chorionic gonadotropin (CG) beta-subunit (1-145 amino
CC   acids) fused to human single chain gonadotropin alpha-subunit (1-92 amino
CC   acids) by a linker sequence. This analog serves as a useful starting
CC   compound for template directed vaccine design and for the development of
CC   hormone-specific vaccines for use in humans.
XX
SQ   Sequence   265 AA;

  Query Match             59.0%;  Score 795;  DB 22;  Length 265;
  Best Local Similarity   99.3%;  Pred. No. 1.5e-58;
  Matches  145;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy    221 KAPPPSLPSPSRLPGPSDTPILPQTS 246
          |||||||||||||||||||||||| |
Db    142 KAPPPSLPSPSRLPGPSDTPILPQGS 167

RESULT 11
AAW93434
ID   AAW93434 standard; peptide; 145 AA.
XX
AC   AAW93434;
XX
DT   11-JUN-1999  (first entry)
XX
DE   Human hCG beta-subunit peptide structure I.
XX
KW   Human chorionic gonadotropin; beta subunit; antigenic peptide; hCG;
KW   contraceptive; vaccine; fertility; polyclonal antisera; diagnostic;
KW   immunogen; human luteinising hormone.
XX
OS   Homo sapiens.
XX
PN   US5891992-A.
XX
PD   06-APR-1999.
XX
PF   06-JUN-1995;   95US-0467569.
XX
PR   07-AUG-1989;   89US-0390530.
PR   04-DEC-1985;   85US-0804642.
PR   17-AUG-1987;   87US-0086401.
PR   06-OCT-1992;   92US-0958601.
PR   06-JUN-1995;   95US-0467569.
XX
PA   (OHIS ) UNIV OHIO STATE RES FOUND.
XX
PI   Stevens VC;
XX
DR   WPI; 1999-253928/21.
XX
PT   Synthetic antigenic peptides from human chorionic gonadotropin
PT   beta-subunit
XX
PS   Disclosure; Column 19; 80pp; English.
XX
CC   This invention describes novel synthetic antigenic peptides (A) based
CC   on the human chorionic gonadotropin (hCG) beta-subunit. These peptides
CC   have contraceptive properties and are used for the development of
CC   vaccines used to control fertility in animals and to generate
CC   polyclonal antisera for diagnostic use. The peptides are more specific
CC   immunogens than corresponding unmodified peptides from hCG beta-subunit,
CC   i.e. they do not elicit antibodies that cross-react with human
CC   luteinising hormone.
XX
SQ   Sequence   145 AA;

  Query Match             58.9%;  Score 793;  DB 20;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-58;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
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Db      2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
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Db     62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy    221 KAPPPSLPSPSRLPGPSDTPILPQ 244
          ||||||||||||||||||||||||
Db    122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 12
AAW95520
ID   AAW95520 standard; protein; 145 AA.
XX
```

```
AC   AAW95520;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Human chorionic gonadotrophin (hCG) beta subunit.
XX
KW   Human; chorionic gonadotropin; hCG; three-dimensional; 3D; analogue;
KW   molecular simulation; visual display; chemical structure; growth factor;
KW   N-glycosylation site; follicle stimulating hormone; luteinising hormone;
KW   thyroid stimulating hormone; in vitro fertilisation; fertility; mutation;
KW   beta subunit; glycoprotein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 64
FT                   /note= "wild-type Phe at this position can be mutated
FT                          to Asn to introduce a new N-glycosylation site;
FT                          see claim 3"
FT   Misc-difference 79
FT                   /note= "wild-type Val at this position can be mutated
FT                          to Asn to introduce a new N-glycosylation site;
FT                          see claim 3"
XX
PN   US5864488-A.
XX
PD   26-JAN-1999.
XX
PF   24-FEB-1995;   95US-0395238.
XX
PR   24-FEB-1994;   94GB-0003600.
XX
PA   (UNIU ) UNIV GLASGOW.
XX
PI   Grootenhuis PDJ,  Harris DC,  Isaacs NW,  Lapthorn AJ;
XX
DR   WPI; 1999-131522/11.
XX
PT   Determining the 3-dimensional coordinates of chorionic gonadotrophin
PT   and computer-assisted re-design of the chemical structure - used for
PT   production of gonadotrophin hormone analogues
XX
PS   Examples; Fig 2; 60pp; English.
XX
CC   The invention relates to determining whether an analogue of human
CC   chorionic gonadotropin (hCG) will have an altered three-dimensional (3D)
CC   structure as compared to hCG. Analogues of hCG and other glycoprotein
CC   hormones are produced by inputting chemical changes to the 3D structure
CC   into a computer loaded with 3D molecular simulation software and
CC   representing visually on a computer display. On inputting into the data
CC   input of the computer at least one operator change in chemical structure
CC   of the hCG molecule, the molecular simulation software produces a
CC   modified 3D molecular representation of the analogue structure. The 3D
CC   representation of the analogue can be displayed on the visual display,
CC   whereby changes in 3D structure of the hCG molecule consequent on changes
CC   in chemical structure can be visually determined. Glycoprotein analogues
CC   with additional glycosylation sites, and analogues with non-essential
CC   hairpins deleted can be produced by this method. The methods can be used
CC   to obtain analogues of hCG, follicle stimulating hormone, luteinising
CC   hormone, thyroid stimulating hormone, which may act as agonists or
CC   antagonists. The analogues can be used as growth factors in mammals, for
CC   in vitro fertilisation techniques and for treatment in vivo to enhance
CC   fertility. The present sequence represents the beta subunit of hCG.
CC   N-glycosylation sites can be introduced by single point mutations at
CC   specified positions to produce hCG analogues.
XX
SQ   Sequence   145 AA;

  Query Match             58.9%;  Score 793;  DB 20;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-58;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy    221 KAPPPSLPSPSRLPGPSDTPILPQ 244
          ||||||||||||||||||||||||
Db    122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 13
AAB20558
ID   AAB20558 standard; protein; 145 AA.
XX
AC   AAB20558;
XX
DT   11-DEC-2000  (first entry)
XX
DE   Human chorionic gonadotropin beta subunit amino acid sequence.
XX
KW   Human; chorionic gonadotropin antigen; follicle stimulating hormone;
KW   contraception; abortion; hormone related disease; carcinoma; cytostatic;
KW   contraceptive; antiinfertility; antihypertensive; antidiabetic; vaccine;
KW   fertility; cancer; hypertension; diabetes.
XX
OS   Homo sapiens.
XX
PN   US6096318-A.
XX
PD   01-AUG-2000.
XX
PF   06-JUN-1995;   95US-0466445.
XX
PR   25-AUG-1978;   78US-0936876.
PR   15-JUL-1987;   87US-0073748.
PR   26-AUG-1992;   92US-0935331.
PR   17-FEB-1989;   89US-0311331.
PR   07-MAY-1973;   73US-0357892.
PR   16-OCT-1973;   73US-0406821.
PR   22-APR-1974;   74US-0462955.
PR   14-OCT-1975;   75US-0622031.
PR   16-JAN-1980;   80US-0112628.
PR   20-NOV-1981;   81US-0323690.
PR   18-MAY-1983;   83WO-US00777.
PR   02-NOV-1984;   84US-0667863.
XX
PA   (OHIS ) UNIV OHIO STATE.
XX
PI   Stevens VC;
XX
DR   WPI; 2000-542298/49.
XX
PT   New antigen for treating hormone related diseases, is conjugated with a
PT   specific polypeptide which elicits an antibody response against human
PT   chorionic gonadotropin  -
XX
PS   Disclosure; Column 18; 61pp; English.
XX
CC   The present invention describes an antigen (A) comprising a carrier
CC   chemically conjugated with a polypeptide (I) capable of eliciting
CC   antibody response to human chorionic gonadotropin (CG) and not to human
CC   luteinising hormone (LH), or a polypeptide (II) capable of eliciting
CC   antibody response to human CG. (A) has cytostatic, contraceptive,
CC   antiinfertility, antihypertensive and antidiabetic activities, and can
CC   be used as part of a vaccine. (A) is useful for contraception, abortion
CC   and for treating hormone related diseases, for treating hormone
CC   associated carcinomas and to boost an animals' resistance to exogenous
CC   proteins e.g. viral proteins. (A) is also useful in animal fertility
CC   control, for treating cancer, hypertension, diabetes and related vascular
CC   diseases. (A), safely and effectively controls various disease states
CC   or maladies caused or influenced by unusual excesses of certain
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CC   polypeptides such as gastrin, angiotensin II or somatomedian. It also
CC   provides an effective and safe method of terminating a pregnancy soon
CC   after conception which does not have serious harmful side effects.
CC   The present sequence represents the human CG beta subunit amino acid
CC   sequence, which is given in the exemplification of the present
CC   invention.
XX
SQ   Sequence   145 AA;

  Query Match             58.9%;  Score 793;  DB 21;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-58;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     221 KAPPPSLPSPSRLPGPSDTPILPQ 244
           ||||||||||||||||||||||||
Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 14
AAU04619
ID   AAU04619 standard; protein; 145 AA.
XX
AC   AAU04619;
XX
DT   23-OCT-2001  (first entry)
XX
DE   Human chorionic gonadotropin (hCG) beta, amino acids 1-145.
XX
KW   Human; chorionic gonadotropin; hCG; glycoprotein hormone; infertility;
KW   luteinising hormone; LH; follicle stimulating hormone; FSH;
KW   thyroid stimulating hormone; TH.
XX
OS   Homo sapiens.
XX
PN   US6242580-B1.
XX
PD   05-JUN-2001.
XX
PF   31-MAR-1999;   99US-0282357.
XX
PR   25-AUG-1997;   97US-0918288.
PR   18-FEB-1994;   94US-0199382.
PR   12-AUG-1994;   94US-0289396.
PR   22-SEP-1994;   94US-0310590.
PR   04-NOV-1994;   94US-0334628.
PR   07-DEC-1994;   94US-0351591.
PR   07-JUN-1995;   95US-0475049.
PR   09-MAY-1997;   97US-0853524.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Boime I,  Moyle WR;
XX
DR   WPI; 2001-424301/45.
XX
PT   New single chain forms of the glycoprotein hormone quartet useful for
PT   generating antibodies specifically immunoreactive with the new
PT   compounds, in treating infertility, or as aids for in vivo
PT   fertilization techniques
XX
PS   Example 19; Column 34; 86pp; English.
XX
CC   The sequence represents the amino acid sequence of human chorionic
CC   gonadotropin (hCG) beta, amino acids 1-145. The protein is an
CC   important glycoprotein hormone heterodimer, along with luteinising
CC   hormone (LH), follicle stimulating hormone (FSH), thyroid stimulating
CC   hormone (TH), which all have identical alpha subunits but differing beta
CC   subunits. The proteins are useful for generating antibodies specifically
CC   immunoreactive with new compounds, as substitutes for the
CC   heterodimeric forms of the hormones, in the treatment of infertility, as
CC   aids for in vivo fertilisation techniques, and in other therapeutic
CC   methods associated with the native hormones. The single chain proteins
CC   are further useful as reagents in a manner similar to the heterodimers,
CC   as diagnostic tools to detect the presence of antibodies with respect to
CC   the native proteins in the biological samples, as control reagents in
CC   assay kits for assessing the levels of these hormones in various samples,
CC   and in detecting and purifying receptors to which the native hormones
CC   bind. The single chain forms of the heterodimers or homodimers have the
CC   following advantages over their dimeric forms: they are more stable,
CC   problems of recombinant production are reduced since only a single gene
CC   is needed to transcribe, translate and process, provide an alternate form
CC   thus permitting fine tuning of activity levels and of in vivo half lives.
CC   Single chain forms are unique starting materials for identifying
CC   truncated forms with the activity of the dimer. The linkage between the
CC   subunits permits the protein to be engineered without disturbing the
CC   overall folding of the protein.
XX
SQ   Sequence   145 AA;

  Query Match             58.9%;  Score 793;  DB 22;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-58;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
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Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
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Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     221 KAPPPSLPSPSRLPGPSDTPILPQ 244
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Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 15
AAE04491
ID   AAE04491 standard; Protein; 145 AA.
XX
AC   AAE04491;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human chorionic gonadotropin beta-subunit fragment (1-145 amino acids).
XX
KW   Human; single chain gonadotropin analog; anti-infertility; drug;
KW   peptide therapy; luteinising hormone; LH; follicle stimulating hormone;
KW   FSH; thyroid stimulating hormone; TSH; chorionic gonadotropin; CG;
KW   glycoprotein; infertility; fusion protein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 145
FT                   /note= "Residue 'O' is present at this location in the
FT                   sequence shown in column 33 of the specification"
XX
PN   US6238890-B1.
XX
PD   29-MAY-2001.
XX
PF   25-AUG-1997;   97US-0918288.
XX
PR   18-FEB-1994;   94US-0199382.
PR   12-AUG-1994;   94US-0289396.
PR   22-SEP-1994;   94US-0310590.
PR   04-NOV-1994;   94US-0334628.
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PR 07-DEC-1994; 94US-0351591.
PR 07-JUN-1995; 95US-0475049.
PR 09-MAY-1997; 97US-0853524.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Boime I, Moyle WR;
XX
DR WPI; 2001-366474/38.
XX
PT New DNA or RNA encoding single chain protein useful in treating
PT infertility, as aids in vitro fertilization techniques, or other
PT therapeutic methods associated with the native hormones -
XX
PS Example 19; Column 103-106; 87pp; English.
XX
CC The invention relates to human single chain forms of the glycoprotein
CC hormone quartet which is an agonist or antagonist of luteinising hormone
CC (LH), follicle stimulating hormone (FSH), thyroid stimulating hormone
CC (TSH) or chorionic gonadotropin (CG). All these hormones are heterodimers
CC having identical alpha subunits and differing beta subunits. The agonist
CC forms of single chain hormones are used in treating infertility, as aids
CC in vitro fertilisation techniques, and other therapeutic methods
CC associated with the native hormones. The single chain hormones are useful
CC as reagents in a manner similar to heterodimers, as diagnostic tools to
CC detect the presence of antibodies with respect to the native proteins in
CC biological samples, as control reagents in assay kits for assessing the
CC levels of these hormones in various samples, in detecting and purifying
CC receptors to which the native hormones bind. The single chain hormones
CC are also used in affinity chromatographic preparation of receptors or
CC antihormone antibodies. They are used as purification tools for
CC isolation of subsequent preparations of these materials and to monitor
CC levels of single chain hormones administered as drugs. The single chain
CC glycoproteins are used to generate antibodies specifically immunoreactive
CC with these new compounds, as substitutes for the heterodimeric forms of
CC hormones. The present sequence is human chorionic gonadotropin beta-
CC subunit fragment (1-145 amino acids) which is used for constructing
CC single chain gonadotropin analogs related to the invention. Analog
CC fusion proteins serves as useful starting compounds for template directed
CC vaccine design and for the development of hormone-specific vaccines for
CC use in humans.
XX
SQ Sequence 145 AA;

Query Match 58.9%; Score 793; DB 22; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.1e-58;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
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Db      2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy    221 KAPPPSLPSPSRLPGPSDTPILPQ 244
          ||||||||||||||||||||||||
Db    122 KAPPPSLPSPSRLPGPSDTPILPQ 145
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Search completed: November 20, 2002, 17:27:36
Job time : 38.1818 secs

OM protein - protein search, using sw model

Run on: November 20, 2002, 17:29:06 ; Search time 8.22378 Seconds
(without alignments)
479.913 Million cell updates/sec

Title: US-09-787-494-4
Perfect score: 1347
Sequence: 1 MRFPSIFTAVLFAASSALAA.....LPGPSDTPILPQTSHHHHHH 252

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	793	58.9	165	9	US-09-915-676-1	Sequence 1, Appli
2	793	58.9	165	10	US-09-466-320-14	Sequence 14, Appl
3	767	56.9	307	10	US-09-756-186-4	Sequence 4, Appli
4	767	56.9	336	10	US-09-756-186-8	Sequence 8, Appli
5	766	56.9	141	9	US-09-813-398-3	Sequence 3, Appli
6	611	45.4	195	10	US-09-780-933-30	Sequence 30, Appl
7	611	45.4	196	10	US-09-780-933-29	Sequence 29, Appl
8	540	40.1	122	9	US-09-813-398-4	Sequence 4, Appli
9	435	32.3	141	10	US-09-730-617-47	Sequence 47, Appl
10	432	32.1	462	10	US-09-846-729A-3	Sequence 3, Appli
11	432	32.1	462	10	US-09-846-729A-17	Sequence 17, Appl
12	432	32.1	464	10	US-09-846-729A-14	Sequence 14, Appl
13	425	31.6	141	10	US-09-730-617-48	Sequence 48, Appl
14	416	30.9	611	10	US-09-829-549A-48	Sequence 48, Appl
15	414.5	30.8	147	10	US-09-740-359-7	Sequence 7, Appli
16	414	30.7	144	10	US-09-894-711-7	Sequence 7, Appli
17	413.5	30.7	144	10	US-09-736-611-6	Sequence 6, Appli
18	413.5	30.7	144	10	US-09-740-359-5	Sequence 5, Appli
19	413.5	30.7	146	10	US-09-894-711-5	Sequence 5, Appli
20	413.5	30.7	147	10	US-09-736-611-8	Sequence 8, Appli
21	403.5	30.0	86	12	US-10-153-064-69	Sequence 69, Appl
22	403	29.9	155	10	US-09-921-398-39	Sequence 39, Appl
23	403	29.9	191	10	US-09-921-398-41	Sequence 41, Appl
24	380	28.2	113	10	US-09-730-617-44	Sequence 44, Appl
25	371	27.5	99	10	US-09-730-617-41	Sequence 41, Appl
26	303	22.5	140	10	US-09-730-617-46	Sequence 46, Appl
27	303	22.5	144	10	US-09-730-617-45	Sequence 45, Appl
28	265.5	19.7	116	10	US-09-730-617-38	Sequence 38, Appl
29	265	19.7	85	10	US-09-730-617-35	Sequence 35, Appl
30	247	18.3	119	9	US-09-813-398-2	Sequence 2, Appli
31	227	16.9	111	9	US-09-973-918A-4	Sequence 4, Appli
32	226	16.8	110	9	US-09-813-398-5	Sequence 5, Appli
33	215	16.0	108	9	US-09-973-918A-11	Sequence 11, Appl
34	215	16.0	109	9	US-09-973-918A-12	Sequence 12, Appl
35	215	16.0	110	9	US-09-973-918A-13	Sequence 13, Appl
36	215	16.0	111	9	US-09-973-918A-6	Sequence 6, Appli
37	215	16.0	111	9	US-09-973-918A-10	Sequence 10, Appl
38	215	16.0	111	10	US-09-780-933-4	Sequence 4, Appli
39	215	16.0	129	10	US-09-780-933-3	Sequence 3, Appli
40	215	16.0	129	10	US-09-780-933-23	Sequence 23, Appl
41	215	16.0	196	10	US-09-780-933-28	Sequence 28, Appl
42	209	15.5	111	9	US-09-973-918A-2	Sequence 2, Appli
43	208	15.4	111	9	US-09-973-918A-8	Sequence 8, Appli
44	204	15.1	38	9	US-09-915-676-3	Sequence 3, Appli
45	204	15.1	38	10	US-09-466-320-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-915-676-1
; Sequence 1, Application US/09915676
; Patent No. US20020164338A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Combined Approach to Treatment of Cancer
; TITLE OF INVENTION: with hCG Vaccines
; FILE REFERENCE: 50450-8027.US01
; CURRENT APPLICATION NUMBER: US/09/915,676
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 09/571,497
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/134,419
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/134,432
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-676-1

Query Match 58.9%; Score 793; DB 9; Length 165;
Best Local Similarity 100.0%; Pred. No. 2.1e-59;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
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Qy    221 KAPPPSLPSPSRLPGPSDTPILPQ 244
          ||||||||||||||||||||||||
Db    142 KAPPPSLPSPSRLPGPSDTPILPQ 165
```

```
RESULT 2
US-09-466-320-14
; Sequence 14, Application US/09466320
; Patent No. US20020025939A1
; GENERAL INFORMATION:
;  APPLICANT: Iversen, Patrick
;  TITLE OF INVENTION: Chorionic Gonadotropin DNA Vaccines and
;  TITLE OF INVENTION: Methods
;  FILE REFERENCE: 0450-0026.30
;  CURRENT APPLICATION NUMBER: US/09/466,320
;  CURRENT FILING DATE: 1999-12-17
;  EARLIER APPLICATION NUMBER: US 60/112,910
;  EARLIER FILING DATE: 1998-12-18
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 165
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: hCG beta sub unit
US-09-466-320-14

  Query Match             58.9%;  Score 793;  DB 10;  Length 165;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-59;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy     221 KAPPPSLPSPSRLPGPSDTPILPQ 244
           ||||||||||||||||||||||||
Db     142 KAPPPSLPSPSRLPGPSDTPILPQ 165


RESULT 3
US-09-756-186-4
; Sequence 4, Application US/09756186
; Patent No. US20010014333A1
;  GENERAL INFORMATION:
;    APPLICANT:  Campbell, Robert K.
;    APPLICANT:  Jameson, Bradford A.
;    APPLICANT:  Chappel, Scott C.
;    TITLE OF INVENTION:  HYBRID PROTEINS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street N.W., Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  22207
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/756,186
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/804,166
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Browdy, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  CAMPBELL-2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  307 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-756-186-4

  Query Match             56.9%;  Score 767;  DB 10;  Length 307;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-57;
  Matches  139;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     106 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     169 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 228

Qy     166 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 225
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     229 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 288

Qy     226 SLPSPSRLPGPSDTPILPQ 244
           ||||||||||||||||||||
Db     289 SLPSPSRLPGPSDTPILPQ 307


RESULT 4
US-09-756-186-8
; Sequence 8, Application US/09756186
; Patent No. US20010014333A1
;  GENERAL INFORMATION:
;    APPLICANT:  Campbell, Robert K.
;    APPLICANT:  Jameson, Bradford A.
;    APPLICANT:  Chappel, Scott C.
;    TITLE OF INVENTION:  HYBRID PROTEINS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street N.W., Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  22207
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/756,186
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/804,166
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Browdy, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  CAMPBELL-2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  336 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-756-186-8
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```
  Query Match             56.9%;  Score 767;  DB 10;  Length 336;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-57;
  Matches  139;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    106 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 165
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    198 PRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFES 257

Qy    166 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 225
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    258 IRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPP 317

Qy    226 SLPSPSRLPGPSDTPILPQ 244
          ||||||||||||||||||||
Db    318 SLPSPSRLPGPSDTPILPQ 336


RESULT 5
US-09-813-398-3
; Sequence 3, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
;  APPLICANT: Bruce D. Weintraub
;  APPLICANT:  Mariusz W. Szkudlinski
;  APPLICANT:  University of Maryland
;  TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
;  FILE REFERENCE: UOFMD.003C1
;  CURRENT APPLICATION NUMBER: US/09/813,398
;  CURRENT FILING DATE:  2001-03-20
;  PRIOR APPLICATION NUMBER: PCT/US99/05908
;  PRIOR FILING DATE: 1999-03-19
;  PRIOR APPLICATION NUMBER: PCT/US98/19772
;  PRIOR FILING DATE: 1998-09-22
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 141
;   TYPE: PRT
;   ORGANISM: HOMO SAPIEN
US-09-813-398-3

  Query Match             56.9%;  Score 766;  DB 9;  Length 141;
  Best Local Similarity   100.0%;  Pred. No. 3e-57;
  Matches  139;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 62

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 122

Qy    221 KAPPPSLPSPSRLPGPSDT 239
          ||||||||||||||||||||
Db    123 KAPPPSLPSPSRLPGPSDT 141


RESULT 6
US-09-780-933-30
; Sequence 30, Application US/09780933
; Patent No. US20020127652A1
; GENERAL INFORMATION:
;  APPLICANT: SCHAMBYE, HANS T.
;  APPLICANT:  ANDERSEN, KIM V.
;  APPLICANT:  VAN DEN HAZEL, BART
;  APPLICANT:  CHRISTIANSEN, JESPER
;  APPLICANT:  JEPPESENT, CLAUS B.
;  TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
;  FILE REFERENCE: 31-001000US
;  CURRENT APPLICATION NUMBER: US/09/780,933
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: PA 2000 00220
;  PRIOR FILING DATE: 2000-02-11
;  PRIOR APPLICATION NUMBER: 60/184,035
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: PA 2000 01092
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: 60/225,558
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
;   LENGTH: 195
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-780-933-30

  Query Match             45.4%;  Score 611;  DB 10;  Length 195;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-44;
  Matches  110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     86 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 145

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 210
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    146 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 195


RESULT 7
US-09-780-933-29
; Sequence 29, Application US/09780933
; Patent No. US20020127652A1
; GENERAL INFORMATION:
;  APPLICANT: SCHAMBYE, HANS T.
;  APPLICANT:  ANDERSEN, KIM V.
;  APPLICANT:  VAN DEN HAZEL, BART
;  APPLICANT:  CHRISTIANSEN, JESPER
;  APPLICANT:  JEPPESENT, CLAUS B.
;  TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
;  FILE REFERENCE: 31-001000US
;  CURRENT APPLICATION NUMBER: US/09/780,933
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: PA 2000 00220
;  PRIOR FILING DATE: 2000-02-11
;  PRIOR APPLICATION NUMBER: 60/184,035
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: PA 2000 01092
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: 60/225,558
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
;   LENGTH: 196
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-780-933-29

  Query Match             45.4%;  Score 611;  DB 10;  Length 196;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-44;
  Matches  110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     87 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 146

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 210
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    147 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD 196


RESULT 8
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US-09-813-398-4
; Sequence 4, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
; APPLICANT: Mariusz W. Szkudlinski
; APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: UOFMD.003C1
; CURRENT APPLICATION NUMBER: US/09/813,398
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 122
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-09-813-398-4

Query Match 40.1%; Score 540; DB 9; Length 122;
Best Local Similarity 85.0%; Pred. No. 1.8e-38;
Matches 96; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
Db 3 REPLRPWCHPINAILAVEKEGCPVCITVNTTICAGYCPTMMRVLQAVLPPLPQVVCTYRD 62

Qy 161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPR 213
Db 63 VRFESIRLPGCPRGVDPVVSFPVALSCRCGPCRRSTSDCGGPKDHPLTCDHPQ 115

RESULT 9
US-09-730-617-47
; Sequence 47, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shimkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: No. US20020068279A1el Proteins and Nucleic Acids Encoding the Sam
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730,617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-730-617-47

Query Match 32.3%; Score 435; DB 10; Length 141;
Best Local Similarity 65.8%; Pred. No. 1.2e-29;
Matches 75; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

Qy 103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
Db 24 PLRPLCQPINATLAAEKEACPVCITFTTSICAGYCPSMKRVLPVILPPMPQRVCTYHELR 83

Qy 163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQD 216
Db 84 FASVRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDHPPLPD 137

RESULT 10
US-09-846-729A-3
; Sequence 3, Application US/09846729A
; Patent No. US20020058322A1
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas
; APPLICANT: Li, Huimin
; APPLICANT: Mann, Michael
; TITLE OF INVENTION: FIBRINOLYTICALLY ACTIVE POLYPEPTIDE
; FILE REFERENCE: A-596
; CURRENT APPLICATION NUMBER: US/09/846,729A
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/411,329
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Native pro-NAT (analog of fibrolase)
US-09-846-729A-3

Query Match 32.1%; Score 432; DB 10; Length 462;
Best Local Similarity 100.0%; Pred. No. 9.7e-29;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSNSTN 60
Db 1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSNSTN 60

Qy 61 NGLLFINTTIASIAAKEEGVSLEKREAEA 89
Db 61 NGLLFINTTIASIAAKEEGVSLEKREAEA 89

RESULT 11
US-09-846-729A-17
; Sequence 17, Application US/09846729A
; Patent No. US20020058322A1
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas
; APPLICANT: Li, Huimin
; APPLICANT: Mann, Michael
; TITLE OF INVENTION: FIBRINOLYTICALLY ACTIVE POLYPEPTIDE
; FILE REFERENCE: A-596
; CURRENT APPLICATION NUMBER: US/09/846,729A
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/411,329
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog form of native pro-fibrolase of Agkistrodon contortrix
US-09-846-729A-17

Query Match 32.1%; Score 432; DB 10; Length 462;
Best Local Similarity 100.0%; Pred. No. 9.7e-29;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSNSTN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSNSTN 60

Qy     61 NGLLFINTTIASIAAKEEGVSLEKREAEA 89
          |||||||||||||||||||||||||||||
Db     61 NGLLFINTTIASIAAKEEGVSLEKREAEA 89


RESULT 12
US-09-846-729A-14
; Sequence 14, Application US/09846729A
; Patent No. US20020058322A1
; GENERAL INFORMATION:
;  APPLICANT: Boone, Thomas
;  APPLICANT:  Li, Huimin
;  APPLICANT:  Mann, Michael
;  TITLE OF INVENTION: FIBRINOLYTICALLY ACTIVE POLYPEPTIDE
;  FILE REFERENCE: A-596
;  CURRENT APPLICATION NUMBER: US/09/846,729A
;  CURRENT FILING DATE:  2001-05-01
;  PRIOR APPLICATION NUMBER: 09/411,329
;  PRIOR FILING DATE: 1999-10-01
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
;   LENGTH: 464
;   TYPE: PRT
;   ORGANISM: Agkistrodon contortrix
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Native pro-fibrolase of Agkistrodon contortrix
US-09-846-729A-14

  Query Match             32.1%;  Score 432;  DB 10;  Length 464;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-29;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSNSTN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSNSTN 60

Qy     61 NGLLFINTTIASIAAKEEGVSLEKREAEA 89
          |||||||||||||||||||||||||||||
Db     61 NGLLFINTTIASIAAKEEGVSLEKREAEA 89


RESULT 13
US-09-730-617-48
; Sequence 48, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
;  APPLICANT: Burgess, Catherine E
;  APPLICANT:  Prayaga, Sudhirdas K
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Zerhusen, Bryan D
;  APPLICANT:  Mezes, Peter S
;  TITLE OF INVENTION: No. US20020068279A1el Proteins and Nucleic Acids Encoding the Sam
;  FILE REFERENCE: 15966-609
;  CURRENT APPLICATION NUMBER: US/09/730,617
;  CURRENT FILING DATE:  2000-12-05
;  PRIOR APPLICATION NUMBER: 60/169,056
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: 60/169,886
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/169,866
;  PRIOR FILING DATE: 1999-12-09
;  PRIOR APPLICATION NUMBER: 60/170,252
;  PRIOR FILING DATE: 1999-12-10
;  PRIOR APPLICATION NUMBER: 60/175,740
;  PRIOR FILING DATE: 2000-01-12
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
;   LENGTH: 141
;   TYPE: PRT
;   ORGANISM: Ovis aries
US-09-730-617-48

  Query Match             31.6%;  Score 425;  DB 10;  Length 141;
  Best Local Similarity   64.9%;  Pred. No. 8.3e-29;
  Matches   74;  Conservative   13;  Mismatches   27;  Indels    0;  Gaps    0;

Qy    103 PLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVR 162
          |||| |:|||||||| ||| ||||||  |:|||||| :| |||  :|| :|| || | ::|
Db     24 PLRPLCQPINATLAAEKEACPVCITFTTSICAGYCLSMKRVLPVILPPMPQRVCTYHELR 83

Qy    163 FESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQD 216
          | |:|||||| ||:|:|:||: ||||| |  || |:||||||:  || || |   |
Db     84 FASVRLPGCPPGVDPMVSFPVALSCHCGPCRLSSTDCGGPRTQPLACDHPPLPD 137


RESULT 14
US-09-829-549A-48
; Sequence 48, Application US/09829549A
; Patent No. US20020052484A1
; GENERAL INFORMATION:
;  APPLICANT: The Curators of the University of Missouri
;  TITLE OF INVENTION: PHAGE DISPLAY SELECTION OF ANTI FUNGAL PEPTIDES
;  FILE REFERENCE: UMO 1521.1
;  CURRENT APPLICATION NUMBER: US/09/829,549A
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: US 60/195,785
;  PRIOR FILING DATE: 2000-04-10
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
;   LENGTH: 611
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)..(85)
;   OTHER INFORMATION: Mat-alpha secretory sequence
;   NAME/KEY: DOMAIN
;   LOCATION: (86)..(600)
;   OTHER INFORMATION: Cytokinin oxidase 1
;   NAME/KEY: DOMAIN
;   LOCATION: (601)..(602)
;   OTHER INFORMATION: Linker
;   NAME/KEY: DOMAIN
;   LOCATION: (603)..(611)
;   OTHER INFORMATION: Random peptide Pc 87
US-09-829-549A-48

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  Best Local Similarity   80.2%;  Pred. No. 3e-27;
  Matches   93;  Conservative    2;  Mismatches   11;  Indels   10;  Gaps    2;

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Db      1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPADAVIGYSDLEGDFDVAVLPFSNSTN 60

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RESULT 15
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; Sequence 7, Application US/09740359
; Patent No. US20010041787A1
; GENERAL INFORMATION:
;  APPLICANT:  Kjeldsen, Thomas Borglum
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;  APPLICANT:  Ludvigsen, Svend
;  TITLE OF INVENTION:  Method for making insulin precursors and
;  TITLE OF INVENTION:  insulin precursor analogues having improved fermentation
;  TITLE OF INVENTION:  yield in yeast
;  FILE REFERENCE:  6148.200-US
;  CURRENT APPLICATION NUMBER: US/09/740,359
;  CURRENT FILING DATE:  2000-12-19
;  PRIOR APPLICATION NUMBER:  PA 2000 00443
;  PRIOR FILING DATE:  2000-03-17
;  PRIOR APPLICATION NUMBER:  PA 1999 01869
;  PRIOR FILING DATE:  1999-12-29
;  PRIOR APPLICATION NUMBER:  60/211,081
;  PRIOR FILING DATE:  2000-06-13
;  PRIOR APPLICATION NUMBER:  60/181,450
;  PRIOR FILING DATE:  2000-02-10
;  NUMBER OF SEQ ID NOS:  16
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 147
;   TYPE: PRT
;   ORGANISM: Alpha leader fused with N-terminally extended
US-09-740-359-7

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  Best Local Similarity   67.3%;  Pred. No. 6.6e-28;
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Qy       1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSNSTN 60
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Db       1 MRFPSIFTAVLFAASSALAAPVNTTTEDETAQIPAEAVIGYSDLEGDFDVAVLPFSNSTN 60

Qy      61 NGLLFINTTIASIAAKEEGVSLEKR---EAEA--YVEFDPGCRDLKEPLRPRCRPINATL 115
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Qy     116 AVEKEGCPVCITVNTTICA-----GYC 137
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Search completed: November 20, 2002, 17:35:35
Job time : 9.22378 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: November 20, 2002, 17:26:27 ; Search time 15.2727 Seconds
(without alignments)
485.478 Million cell updates/sec

Title: US-09-787-494-4
Perfect score: 1347
Sequence: 1 MRFPSIFTAVLFAASSALAA.....LPGPSDTPILPQTSHHHHHH 252

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	795	59.0	265	4	US-08-918-288-3	Sequence 3, Appli
2	795	59.0	265	4	US-08-918-288-39	Sequence 39, Appl
3	795	59.0	265	4	US-09-282-357-3	Sequence 3, Appli
4	795	59.0	265	4	US-09-282-357-39	Sequence 39, Appl
5	793	58.9	145	1	US-08-475-213-10	Sequence 10, Appl
6	793	58.9	145	2	US-08-395-238-2	Sequence 2, Appli
7	793	58.9	145	4	US-09-142-320-12	Sequence 12, Appl
8	793	58.9	145	4	US-09-142-320-13	Sequence 13, Appl
9	793	58.9	145	4	US-09-142-320-14	Sequence 14, Appl
10	793	58.9	145	4	US-09-142-320-15	Sequence 15, Appl
11	793	58.9	145	4	US-08-918-288-68	Sequence 68, Appl
12	793	58.9	145	4	US-09-282-357-68	Sequence 68, Appl
13	793	58.9	145	4	US-08-908-371B-1	Sequence 1, Appli
14	790	58.6	165	2	US-08-709-924-2	Sequence 2, Appli
15	790	58.6	165	2	US-08-709-925-2	Sequence 2, Appli
16	790	58.6	165	4	US-08-709-948-2	Sequence 2, Appli
17	789	58.6	181	4	US-08-918-288-36	Sequence 36, Appl
18	789	58.6	181	4	US-09-282-357-36	Sequence 36, Appl
19	787	58.4	145	1	US-08-425-673-1	Sequence 1, Appli
20	787	58.4	145	1	US-08-425-673-2	Sequence 2, Appli
21	787	58.4	145	1	US-08-298-189B-1	Sequence 1, Appli
22	785	58.3	145	4	US-09-142-320-16	Sequence 16, Appl
23	773	57.4	145	4	US-09-142-320-11	Sequence 11, Appl
24	772	57.3	145	4	US-09-142-320-4	Sequence 4, Appli
25	767	56.9	307	4	US-08-804-166-4	Sequence 4, Appli
26	767	56.9	307	4	US-08-910-991-4	Sequence 4, Appli
27	767	56.9	336	4	US-08-804-166-8	Sequence 8, Appli
28	767	56.9	336	4	US-08-910-991-8	Sequence 8, Appli
29	766	56.9	145	1	US-08-425-673-10	Sequence 10, Appl
30	644	47.8	234	4	US-08-918-288-6	Sequence 6, Appli
31	644	47.8	234	4	US-09-282-357-6	Sequence 6, Appli
32	629	46.7	114	4	US-08-918-288-69	Sequence 69, Appl
33	629	46.7	114	4	US-09-282-357-69	Sequence 69, Appl
34	578	42.9	234	4	US-08-918-288-24	Sequence 24, Appl
35	578	42.9	234	4	US-09-282-357-24	Sequence 24, Appl
36	565	41.9	114	1	US-08-425-673-9	Sequence 9, Appli
37	557	41.4	114	1	US-08-425-673-7	Sequence 7, Appli
38	555	41.2	234	4	US-08-918-288-9	Sequence 9, Appli
39	555	41.2	234	4	US-09-282-357-9	Sequence 9, Appli
40	549	40.8	234	4	US-08-918-288-21	Sequence 21, Appl
41	549	40.8	234	4	US-09-282-357-21	Sequence 21, Appl
42	545	40.5	237	4	US-08-918-288-18	Sequence 18, Appl
43	545	40.5	237	4	US-09-282-357-18	Sequence 18, Appl
44	540	40.1	114	4	US-08-918-288-71	Sequence 71, Appl
45	540	40.1	114	4	US-09-282-357-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-08-918-288-3
; Sequence 3, Application US/08918288
; Patent No. 6238890
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,288
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/282,357
; FILING DATE:
; APPLICATION NUMBER: 08/853,524
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 08/199,382
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20050.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-887-0763
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-918-288-3

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  Query Match           59.0%;  Score 795;  DB 4;  Length 265;
  Best Local Similarity  99.3%;  Pred. No. 2.5e-67;
  Matches  145;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
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Db     22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
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Qy    221 KAPPPSLPSPSRLPGPSDTPILPQTS 246
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Db    142 KAPPPSLPSPSRLPGPSDTPILPQGS 167


RESULT 2
US-08-918-288-39
; Sequence 39, Application US/08918288
; Patent No. 6238890
;  GENERAL INFORMATION:
;    APPLICANT:  BOIME, Irving
;    APPLICANT:  MOYLE, William R.
;    TITLE OF INVENTION:  SINGLE-CHAIN FORMS OF THE
;    TITLE OF INVENTION:  GLYCOPROTEIN HORMONE QUARTET
;    NUMBER OF SEQUENCES:  83
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/918,288
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/282,357
;      FILING DATE:
;      APPLICATION NUMBER:  08/853,524
;      FILING DATE:  09-MAY-1997
;      APPLICATION NUMBER:  08/199,382
;      FILING DATE:  18-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  29500-20050.25
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-887-0763
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  265 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-08-918-288-39

  Query Match           59.0%;  Score 795;  DB 4;  Length 265;
  Best Local Similarity  99.3%;  Pred. No. 2.5e-67;
  Matches  145;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
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Db     22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
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Qy    221 KAPPPSLPSPSRLPGPSDTPILPQTS 246
          ||||||||||||||||||||||| | |
Db    142 KAPPPSLPSPSRLPGPSDTPILPQGS 167


RESULT 3
US-09-282-357-3
; Sequence 3, Application US/09282357
; Patent No. 6242580
;  GENERAL INFORMATION:
;    APPLICANT:  BOIME, Irving
;    APPLICANT:  MOYLE, William R.
;    TITLE OF INVENTION:  SINGLE-CHAIN FORMS OF THE
;    TITLE OF INVENTION:  GLYCOPROTEIN HORMONE QUARTET
;    NUMBER OF SEQUENCES:  83
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/282,357
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/918,288
;      FILING DATE:  25 AUG-1997
;      APPLICATION NUMBER:  08/853,524
;      FILING DATE:  09-MAY-1997
;      APPLICATION NUMBER:  08/199,382
;      FILING DATE:  18-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  29500-20050.25
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-887-0763
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  265 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-09-282-357-3

  Query Match           59.0%;  Score 795;  DB 4;  Length 265;
  Best Local Similarity  99.3%;  Pred. No. 2.5e-67;
  Matches  145;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db     22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
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Qy    221 KAPPPSLPSPSRLPGPSDTPILPQTS 246
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Db    142 KAPPPSLPSPSRLPGPSDTPILPQGS 167


RESULT 4
US-09-282-357-39
; Sequence 39, Application US/09282357
; Patent No. 6242580
;  GENERAL INFORMATION:
;    APPLICANT:  BOIME, Irving
;    APPLICANT:  MOYLE, William R.
;    TITLE OF INVENTION:  SINGLE-CHAIN FORMS OF THE
;    TITLE OF INVENTION:  GLYCOPROTEIN HORMONE QUARTET
;    NUMBER OF SEQUENCES:  83
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/282,357
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/918,288
;      FILING DATE:  25 AUG-1997
;      APPLICATION NUMBER:  08/853,524
;      FILING DATE:  09-MAY-1997
;      APPLICATION NUMBER:  08/199,382
;      FILING DATE:  18-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  29500-20050.25
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-887-0763
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  265 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
US-09-282-357-39

  Query Match             59.0%;  Score 795;  DB 4;  Length 265;
  Best Local Similarity   99.3%;  Pred. No. 2.5e-67;
  Matches  145;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy    221 KAPPPSLPSPSRLPGPSDTPILPQTS 246
          |||||||||||||||||||||||| |
Db    142 KAPPPSLPSPSRLPGPSDTPILPQGS 167


RESULT 5
US-08-475-213-10
; Sequence 10, Application US/08475213
; Patent No. 5783674
;  GENERAL INFORMATION:
;    APPLICANT:  Geysen, Hendrik M.
;    TITLE OF INVENTION:  Method for the use and Synthesis of
;    TITLE OF INVENTION:  Peptides
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Chiron Corporation
;      STREET:  4560 Horton Street
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94608
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,213
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/752,437
;      FILING DATE:  06-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO pct/au90/00062
;      FILING DATE:  16-FEB-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PJ2788/89
;      FILING DATE:  17-FEB-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Green, Grant D.
;      REGISTRATION NUMBER:  31259
;      REFERENCE/DOCKET NUMBER:  0240.002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-601-2706
;      TELEFAX:  510-655-3542
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  145 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-475-213-10

  Query Match             58.9%;  Score 793;  DB 1;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-67;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy    221 KAPPPSLPSPSRLPGPSDTPILPQ 244
          ||||||||||||||||||||||||
Db    122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 6
US-08-395-238-2
; Sequence 2, Application US/08395238
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; Patent No. 5864488
;  GENERAL INFORMATION:
;    APPLICANT:  ISSACS, Neil William
;    APPLICANT:  LAPTHORN, Adrian Jonathan
;    APPLICANT:  HARRIS, Deborah Claire
;    TITLE OF INVENTION:  THREE DIMENSIONAL HORMONE STRUCTURE
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AKZO NOBEL PATENT DEPARTMENT
;      STREET:  1300 PICCARD DRIVE, SUITE 206
;      CITY:  ROCKVILLE
;      STATE:  MARYLAND
;      COUNTRY:  UNITED STATES
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/395,238
;      FILING DATE:  24-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9403600.1
;      FILING DATE:  24-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WILLIAM M. BLACKSTONE
;      REGISTRATION NUMBER:  29,722
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  145 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      STRAIN:  BETA-SUBUNIT HUMAN CHORIONIC GONADOTROPIN
US-08-395-238-2

  Query Match             58.9%;  Score 793;  DB 2;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-67;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
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Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
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Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     221 KAPPPSLPSPSRLPGPSDTPILPQ 244
           ||||||||||||||||||||||||
Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 7
US-09-142-320-12
; Sequence 12, Application US/09142320
; Patent No. 6194154
; GENERAL INFORMATION:
;  APPLICANT: Bellet, Dominique
;  APPLICANT: Bidart, Jean-Michel
;  APPLICANT: Vidaud, Michel
;  APPLICANT: Lazar, Vladimir
;  TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION  DETECTION METHOD
;  FILE REFERENCE: 065691/0140
;  CURRENT APPLICATION NUMBER: US/09/142,320
;  CURRENT FILING DATE: 1998-09-04
;  EARLIER APPLICATION NUMBER: PCT/FR97/00361
;  EARLIER FILING DATE: 1997-02-28
;  EARLIER APPLICATION NUMBER: FR 96 02683
;  EARLIER FILING DATE: 1996-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 145
;   TYPE: PRT
;   ORGANISM: human
US-09-142-320-12

  Query Match             58.9%;  Score 793;  DB 4;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-67;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
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Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
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Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     221 KAPPPSLPSPSRLPGPSDTPILPQ 244
           ||||||||||||||||||||||||
Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 8
US-09-142-320-13
; Sequence 13, Application US/09142320
; Patent No. 6194154
; GENERAL INFORMATION:
;  APPLICANT: Bellet, Dominique
;  APPLICANT: Bidart, Jean-Michel
;  APPLICANT: Vidaud, Michel
;  APPLICANT: Lazar, Vladimir
;  TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION  DETECTION METHOD
;  FILE REFERENCE: 065691/0140
;  CURRENT APPLICATION NUMBER: US/09/142,320
;  CURRENT FILING DATE: 1998-09-04
;  EARLIER APPLICATION NUMBER: PCT/FR97/00361
;  EARLIER FILING DATE: 1997-02-28
;  EARLIER APPLICATION NUMBER: FR 96 02683
;  EARLIER FILING DATE: 1996-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 145
;   TYPE: PRT
;   ORGANISM: human
US-09-142-320-13

  Query Match             58.9%;  Score 793;  DB 4;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-67;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     221 KAPPPSLPSPSRLPGPSDTPILPQ 244
           ||||||||||||||||||||||||
Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 9
US-09-142-320-14
; Sequence 14, Application US/09142320
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; Patent No. 6194154
; GENERAL INFORMATION:
;  APPLICANT: Bellet, Dominique
;  APPLICANT: Bidart, Jean-Michel
;  APPLICANT: Vidaud, Michel
;  APPLICANT: Lazar, Vladimir
;  TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION  DETECTION METHOD
;  FILE REFERENCE: 065691/0140
;  CURRENT APPLICATION NUMBER: US/09/142,320
;  CURRENT FILING DATE: 1998-09-04
;  EARLIER APPLICATION NUMBER: PCT/FR97/00361
;  EARLIER FILING DATE: 1997-02-28
;  EARLIER APPLICATION NUMBER: FR 96 02683
;  EARLIER FILING DATE: 1996-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 145
;   TYPE: PRT
;   ORGANISM: human
US-09-142-320-14

  Query Match             58.9%;  Score 793;  DB 4;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-67;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
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Db      2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy    221 KAPPPSLPSPSRLPGPSDTPILPQ 244
          ||||||||||||||||||||||||
Db    122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 10
US-09-142-320-15
; Sequence 15, Application US/09142320
; Patent No. 6194154
; GENERAL INFORMATION:
;  APPLICANT: Bellet, Dominique
;  APPLICANT: Bidart, Jean-Michel
;  APPLICANT: Vidaud, Michel
;  APPLICANT: Lazar, Vladimir
;  TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION  DETECTION METHOD
;  FILE REFERENCE: 065691/0140
;  CURRENT APPLICATION NUMBER: US/09/142,320
;  CURRENT FILING DATE: 1998-09-04
;  EARLIER APPLICATION NUMBER: PCT/FR97/00361
;  EARLIER FILING DATE: 1997-02-28
;  EARLIER APPLICATION NUMBER: FR 96 02683
;  EARLIER FILING DATE: 1996-03-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 145
;   TYPE: PRT
;   ORGANISM: human
US-09-142-320-15

  Query Match             58.9%;  Score 793;  DB 4;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-67;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
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Db     62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy    221 KAPPPSLPSPSRLPGPSDTPILPQ 244
          ||||||||||||||||||||||||
Db    122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 11
US-08-918-288-68
; Sequence 68, Application US/08918288
; Patent No. 6238890
;  GENERAL INFORMATION:
;    APPLICANT:  BOIME, Irving
;    APPLICANT:  MOYLE, William R.
;    TITLE OF INVENTION:  SINGLE-CHAIN FORMS OF THE
;    TITLE OF INVENTION:  GLYCOPROTEIN HORMONE QUARTET
;    NUMBER OF SEQUENCES:  83
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/918,288
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/282,357
;      FILING DATE:
;      APPLICATION NUMBER:  08/853,524
;      FILING DATE:  09-MAY-1997
;      APPLICATION NUMBER:  08/199,382
;      FILING DATE:  18-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  29500-20050.25
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-887-0763
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  145 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-918-288-68

  Query Match             58.9%;  Score 793;  DB 4;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-67;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy    221 KAPPPSLPSPSRLPGPSDTPILPQ 244
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Db    122 KAPPPSLPSPSRLPGPSDTPILPQ 145
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RESULT 12
US-09-282-357-68
; Sequence 68, Application US/09282357
; Patent No. 6242580
;  GENERAL INFORMATION:
;    APPLICANT:  BOIME, Irving
;    APPLICANT:  MOYLE, William R.
;    TITLE OF INVENTION:  SINGLE-CHAIN FORMS OF THE
;    TITLE OF INVENTION:  GLYCOPROTEIN HORMONE QUARTET
;    NUMBER OF SEQUENCES:  83
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/282,357
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/918,288
;      FILING DATE:  25 AUG-1997
;      APPLICATION NUMBER:  08/853,524
;      FILING DATE:  09-MAY-1997
;      APPLICATION NUMBER:  08/199,382
;      FILING DATE:  18-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  29500-20050.25
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-887-0763
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  145 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-282-357-68

  Query Match             58.9%;  Score 793;  DB 4;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-67;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
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Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
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Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     221 KAPPPSLPSPSRLPGPSDTPILPQ 244
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Db     122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 13
US-08-908-371B-1
; Sequence 1, Application US/08908371B
; Patent No. 6331610
;  GENERAL INFORMATION:
;    APPLICANT:  Bourinbaiar, Aldar S.
;    TITLE OF INVENTION:  A Method for Preventing and Treating
;    TITLE OF INVENTION:  AIDS and HIV Infection Using Select Peptides From the
;    TITLE OF INVENTION:  Beta Subunit of Human Chorionic Gonadotropin
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Metatron, Inc.
;      STREET:  367 Bay Shore Road
;      CITY:  Deer Park
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  11729
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 in. diskette (1.44megabytes)
;      COMPUTER:  IBM Compatible PC
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WORD 6.0  ASCII TEXT CONVERSION ONLY
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/908,371B
;      FILING DATE:  07-AUG-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/044,937
;      FILING DATE:  25-APR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COLEMAN, HENRY D.
;      REGISTRATION NUMBER:  32,559
;      REFERENCE/DOCKET NUMBER:  M31-013
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 679-0090
;      TELEFAX:  (212) 679-9121
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  145 Amino Acid Units
;      TYPE:  Amino Acid
;      STRANDEDNESS:  Single Stranded
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  Protein Subunit
;      DESCRIPTION:  Amino Acid Corresponding to Beta Subunit
;      DESCRIPTION:  of Human Chorionic Gonadotropin
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:  Sequence
;    IMMEDIATE SOURCE:  N/A
;    POSITION IN GENOME:  N/A
;    FEATURE:
;      NAME/KEY:  145 Units of Beta Subunit of Human Chorionic
;      NAME/KEY:  Gonadotropin
;      LOCATION:  N/A
;      IDENTIFICATION METHOD:  Sequencing
;    PUBLICATION INFORMATION:
;      AUTHORS:  CARLSEN, Robert B.,
;      AUTHORS:  BAHL, Ohm P.
;      AUTHORS:  SWAMINATHAN, N.
;      TITLE:  HUMAN CHORIONIC GONADOTROPIN
;      JOURNAL:  THE JOURNAL OF BIOLOGICAL CHEMISTRY
;      VOLUME:  248
;      PAGES:  6810-6825
;      DATE:  1973
US-08-908-371B-1

  Query Match             58.9%;  Score 793;  DB 4;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-67;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 61

Qy     161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
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Db      62 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 121

Qy     221 KAPPPSLPSPSRLPGPSDTPILPQ 244
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Db    122 KAPPPSLPSPSRLPGPSDTPILPQ 145


RESULT 14
US-08-709-924-2
; Sequence 2, Application US/08709924
; Patent No. 5968513
;  GENERAL INFORMATION:
;    APPLICANT:  Gallo, Robert C.
;    APPLICANT:  Bryant, Joseph
;    APPLICANT:  Lunardi-Iskandar, Yanto
;    TITLE OF INVENTION:  METHODS OF PROMOTING HEMATOPOIESIS
;    TITLE OF INVENTION:  USING DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,924
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  8769-018
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  165 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-709-924-2

  Query Match             58.6%;  Score 790;  DB 2;  Length 165;
  Best Local Similarity   99.3%;  Pred. No. 3.9e-67;
  Matches  143;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
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Db     22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
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Db     82 VRFESIRLPGCPRGLNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy    221 KAPPPSLPSPSRLPGPSDTPILPQ 244
          ||||||||||||||||||||||||
Db    142 KAPPPSLPSPSRLPGPSDTPILPQ 165


RESULT 15
US-08-709-925-2
; Sequence 2, Application US/08709925
; Patent No. 5997871
;  GENERAL INFORMATION:
;    APPLICANT:  Gallo, Robert C.
;    APPLICANT:  Bryant, Joseph
;    APPLICANT:  Lunardi-Iskandar, Yanto
;    TITLE OF INVENTION:  TREATMENT AND PREVENTION OF CANCER BY
;    TITLE OF INVENTION:  ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROP
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,925
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  512
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Misrock, S. Leslie
;      REGISTRATION NUMBER:  18,872
;      REFERENCE/DOCKET NUMBER:  8769-017
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
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;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  165 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-709-925-2

  Query Match             58.6%;  Score 790;  DB 2;  Length 165;
  Best Local Similarity   99.3%;  Pred. No. 3.9e-67;
  Matches  143;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    101 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 160
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Db     22 KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRD 81

Qy    161 VRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 220
          ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db     82 VRFESIRLPGCPRGLNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCDDPRFQDSSSS 141

Qy    221 KAPPPSLPSPSRLPGPSDTPILPQ 244
          ||||||||||||||||||||||||
Db    142 KAPPPSLPSPSRLPGPSDTPILPQ 165


Search completed: November 20, 2002, 17:29:32
Job time : 15.2727 secs
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